

**PHARMACEUTICAL PREPARATIONS AND METHODS
FOR INHIBITING TUMORS**

5

FIELD OF THE INVENTION

The present invention relates to pharmaceutical preparations (i.e., composition) for use as tumor suppressive agents for tumors arising from cancers such as prostatic adenocarcinoma, stomach
10 cancer, breast cancer, endometrial and ovarian cancers, and benign prostate hyperplasia (BPH).

BACKGROUND OF THE INVENTION

15 The prostate gland, which is found exclusively in male mammals, produces several components of semen and blood and several regulatory peptides. The prostate gland comprises stroma and epithelium cells, the latter group consisting of columnar secretory cells and basal nonsecretory cells. A proliferation of these basal cells as well as
20 stroma cells gives rise to benign prostatic hyperplasia (BPH), which is one common prostate disease. Another common prostate disease is prostatic adenocarcinoma (CaP), which is the most common of the fatal pathophysiological prostate cancers, and involves a malignant transformation of epithelial cells in the peripheral region of the
25 prostate gland. Prostatic adenocarcinoma and benign prostatic hyperplasia are two common prostate diseases, which have a high rate of incidence in the aging human male population. Approximately one out of every four males above the age of 55 suffers from a prostate disease of some form or another. Prostate cancer is the second most
30 common cause of cancer related death in elderly men, with approximately 96,000 cases diagnosed and about 26,000 deaths reported annually in the United States.

35 Studies of the various substances synthesized and secreted by normal, benign and cancerous prostates carried out in order to gain an understanding of the pathogenesis of the various prostate diseases reveal that certain of these substances may be used as immunohistochemical tumor markers in the diagnosis of prostate disease. The three predominant proteins or polypeptides secreted by
40 a normal prostate gland are: (1) Prostatic Acid Phosphatase (PAP); (2) Prostate Specific Antigen (PSA); and, (3) Prostate Secretory Protein of 94 amino acids (PSP94), which is also known as Prostatic Inhibin Peptide (PIP), Human Seminal Plasma Inhibin (HSPI), or β -

microseminoprotein (β -MSP), and which is hereinafter referred to as PSP94.

5 PSP94 is a simple non-glycosylated cysteine-rich protein, and
constitutes one of three predominant proteins found in human seminal
fluid along with Prostate Specific Antigen (PSA) and Prostate Acid
Phosphatase (PAP). PSP94 has a molecular weight of 10.7 kiloDalton
(kDa), and the complete amino acid sequence of this protein has
already been determined (SEQ ID NO:1). The cDNA and gene for PSP94
10 have been cloned and characterized (Ulvback, et al., Biochem.
Biophys. Res. Comm., 164:1310, 1989; Green, et al., Biochem. Biophys.
Res. Comm., 167:1184, 1990). Immunochemical and in situ
hybridization techniques have shown that PSP94 is located
predominantly in prostate epithelial cells. It is also present,
15 however, in a variety of other secretory epithelial cells (Weiber, et
al., Am. J. Pathol., 137:593, 1990). PSP94 has been shown to be
expressed in prostate adenocarcinoma cell line, LNCap (Yang, et al.,
J. Urol., 160:2240, 1998). As well, an inhibitory effect of
exogenous PSP94 on tumor cell growth has been observed both in vivo
20 and in vitro (Garde, et al., Prostate, 22:225, 1993; Lokeshwar, et
al., Cancer Res., 53:4855, 1993), suggesting that PSP94 could be a
negative regulator for prostate carcinoma growth via interaction with
cognate receptors on tumor cells.

25 Native PSP94 has been shown to have a therapeutic modality in
treating hormone refractory prostate cancer (and potentially other
prostate indications).

Metabolic and immunohistochemical studies have shown that the
30 prostate is a major source of PSP94. PSP94 is involved in the
feedback control of, and acts to suppress secretion of, circulating
follicle-stimulating hormone (FSH) both in-vitro and in-vivo in adult
male rats. PSP94 acts both at the pituitary as well as at the
prostate site since both are provided with receptor sites for PSP94.
35 It has been demonstrated to suppress the biosynthesis and release of
FSH from the rat pituitary as well as to possibly affect the
synthesis/secretion of an FSH-like peptide by the prostate. These
findings suggest that the effects of PSP-94 on tumor growth in vivo,
could be attributed to the reduction in serum FSH levels.

40 Both PSA and PAP have been studied as tumor markers in the
detection of prostate disease, but since both exhibit elevated levels
in prostates having benign prostatic hyperplasia (BPH), neither
marker is specific and therefore they are of limited utility.

Recently, it has been shown that PSP94 concentrations in serum of patients with BPH or CaP are significantly higher than normal. The highest serum concentration of PSP94 observed in normal men is approximately 40 ng/ml, while in men with either BPH or CaP, serum concentrations of PSP94 have been observed in the range from 300-400 ng/ml. Because there exists some overlap in the concentrations of PSP94 in subjects having normal prostates and patients exhibiting either BPH or CaP, serum levels in and of themselves are of little value.

A major therapy in the treatment of prostate cancer is androgen-ablation. While most patients respond initially to this treatment, its effectiveness decreases over time, possibly because of the presence of a heterogenous population of androgen-dependant and androgen-independent cells to the androgen treatment, while any androgen insensitive cells present would continue to proliferate unabated.

Other forms of cancer, which are currently exacting a heavy toll on population are breast cancer in women and cancer of the gastrointestinal tract. Currently, the use of various cancer drugs such as mitomycin, idarubicin, cisplatin, 5-fluoro-uracil, methotrexate, adriamycin and daunomycin form part of the therapy for treating such cancers. One drawback to such a therapeutic treatment is the presence of adverse side effects due to the drugs in the concentration ranges required for effective treatment.

Accordingly, it would be advantageous to find a more effective means of arresting the growth of prostate, breast and gastrointestinal cancer cells and tumors, which may be used effectively against both androgen sensitive and androgen insensitive cells.

In previous work, described in United States Patent No. 5,428,011, we provided pharmaceutical preparations (i.e., compositions) of native human seminal plasma PSP94 for inhibiting in-vitro and in-vivo cancerous prostate, gastrointestinal and breast tumors. The pharmaceutical preparations included native human seminal plasma PSP94 which could be administered in an appropriate dosage form, dosage quantity and dosage regimen to a patient suffering from prostate cancer. In another embodiment, the pharmaceutical preparation included a mixture of human seminal plasma PSP94 and an anticancer drug which may be administered in an

appropriate dosage form, dosage quantity and dosage regimen to a patient suffering from, for example gastrointestinal cancer.

5 PSP94 sourced from human seminal fluid carries with it
significant risk of contamination with infectious agents (e.g., HIV, hepatitis (a, b, or c), and other viruses and/or prions). Even with the use of harsh chemical treatment, total eradication of such agents cannot be guaranteed. Additionally, human seminal fluid is found in limited supply, thus making bulk production of PSP94 very difficult.
10 Therefore, the acceptability of human or even xenogeneic sourced PSP94 may be very difficult for both the regulatory authorities and the marketplace.

Therefore, the use of recombinant technology for producing
15 PSP94 would represent a significant advancement, as recombinant PSP94 could be produced both free of pathogens and in an unlimited supply. Furthermore, the material would be homogeneous from a single lot source, avoiding batch variation.

20 SUMMARY OF THE INVENTION

In its first aspect the present invention relates to a polypeptide or a polypeptide analog selected from the group
25 consisting of the polypeptide as set forth in SEQ ID NO: 3, the polypeptide as set forth in SEQ ID NO: 4, the polypeptide as set forth in SEQ ID NO: 5, and the polypeptide as set forth in SEQ ID NO: 6, a polypeptide analog of at least five contiguous amino acids of SEQ ID NO: 2, of SEQ ID NO: 3, of SEQ ID NO: 4, of SEQ ID NO: 5, or
30 of SEQ ID NO: 6, a polypeptide analog of at least two contiguous amino acids of SEQ ID NO: 2, of SEQ ID NO: 3, of SEQ ID NO: 4, of SEQ ID NO: 5, or of SEQ ID NO: 6, a polypeptide analog consisting of the amino acid sequence $X_1 W Q X_2 D X_1 C X_1 X_2 C X_2 C X_3 X_1 X_2$ as set forth in SEQ ID NO: 89, wherein X_1 is either glutamic acid (Glu), asparagine
35 (Asn) or aspartic acid (Asp), X_2 is either threonine (Thr) or serine (Ser), and X_3 is either tyrosine (Tyr) or phenylalanine (Phe), a polypeptide analog comprising SEQ ID NO: 5 and having an addition of at least one amino acid to its amino-terminus, wherein said
polypeptide analog comprising SEQ ID NO:5 is selected from the group
40 consisting of SEQ ID NO: 59 to SEQ ID NO: 88, a polypeptide analog comprising SEQ ID NO: 5 and having an addition of at least one amino acid to its carboxy-terminus, wherein said polypeptide analog comprising SEQ ID NO:5 is selected from the group consisting of SEQ ID NO: 10 to SEQ ID NO: 58, a polypeptide analog comprising two to

fifty units of SEQ ID NO: 5, a polypeptide analog comprising two to ten units of SEQ ID NO: 5, a polypeptide analog consisting of a sequence of from two to fourteen amino acid units wherein the amino acid units are selected from the group of amino acid units of SEQ ID NO: 5 consisting of glutamic acid (Glu), tryptophan (Trp), glutamine (Gln), threonine (Thr), aspartic acid (Asp), asparagine (Asn), cysteine (Cys), or tyrosine (Tyr), a polypeptide analog having at least 90 % of its amino acid sequence identical to the amino acid sequence set forth in SEQ ID NO: 5, a polypeptide analog having at least 70 % of its amino acid sequence identical to the amino acid sequence set forth in SEQ ID NO: 5, and a polypeptide analog having at least 50 % of its amino acid sequence identical to the amino acid sequence set forth in SEQ ID NO: 5. The polypeptide analog mentioned herein may be capable of inhibiting the growth of a tumor or more precisely may be capable of inhibiting the growth of prostatic adenocarcinoma, stomach cancer, breast cancer, endometrial, ovarian or other cancers of epithelial secretion, or benign prostate hyperplasia (BPH).

In a second aspect, the present invention relates to the use of a polypeptide or a polypeptide analog selected from the group consisting of rHuPSP94 as set forth in SEQ ID NO: 2, the decapeptide as set forth in SEQ ID NO: 3, the polypeptide as set forth in SEQ ID NO: 4 (polypeptide 7-21), the polypeptide as set forth in SEQ ID NO: 5 (PCK3145), and the polypeptide as set forth in SEQ ID NO: 6 (polypeptide 76-94), a polypeptide analog of at least five contiguous amino acids of SEQ ID NO: 2, of SEQ ID NO: 3, of SEQ ID NO: 4, of SEQ ID NO: 5, or of SEQ ID NO: 6, a polypeptide analog of at least two contiguous amino acids of SEQ ID NO: 2, of SEQ ID NO: 3, of SEQ ID NO: 4, of SEQ ID NO: 5, or of SEQ ID NO: 6, a polypeptide analog consisting of the amino acid sequence $X_1 W Q X_2 D X_1 C X_1 X_2 C X_2 C X_3 X_1 X_2$ as set forth in SEQ ID NO: 89, wherein X_1 is either glutamic acid (Glu), asparagine (Asn) or aspartic acid (Asp), X_2 is either threonine (Thr) or serine (Ser), and X_3 is either tyrosine (Tyr) or phenylalanine (Phe), a polypeptide analog comprising SEQ ID NO: 5 and having an addition of at least one amino acid to its amino-terminus, wherein said polypeptide analog comprising SEQ ID NO: 5 is selected from the group consisting of SEQ ID NO: 59 to SEQ ID NO: 88, a polypeptide analog comprising SEQ ID NO: 5 and having an addition of at least one amino acid to its carboxy-terminus, wherein said polypeptide analog comprising SEQ ID NO: 5 is selected from the group consisting of SEQ ID NO: 10 to SEQ ID NO: 58, a polypeptide analog comprising two to fifty units of SEQ ID NO: 5, a polypeptide analog comprising two to ten units of SEQ ID NO: 5, a polypeptide analog

consisting of a sequence of from two to fourteen amino acid units wherein the amino acid units are selected from the group of amino acid units of SEQ ID NO: 5 consisting of glutamic acid (Glu), tryptophan (Trp), glutamine (Gln), threonine (Thr), aspartic acid (Asp), asparagine (Asn), cysteine (Cys), or tyrosine (Tyr), a polypeptide analog having at least 90 % of its amino acid sequence identical to the amino acid sequence set forth in SEQ ID NO: 5, a polypeptide analog having at least 70 % of its amino acid sequence identical to the amino acid sequence set forth in SEQ ID NO: 5, and a polypeptide analog having at least 50 % of its amino acid sequence identical to the amino acid sequence set forth in SEQ ID NO: 5 and mixture(s) thereof, for inhibiting the growth of a tumor or more precisely for inhibiting the growth of prostatic adenocarcinoma, stomach cancer, breast cancer, endometrial, ovarian or other cancers of epithelial secretion, or benign prostate hyperplasia (BPH).

In one embodiment of the second aspect of the present invention, the polypeptide or polypeptide analog may be used with an anticancer drug, such as, for example, mitomycin, idarubicin, cisplatin, 5-fluoro-uracil, methotrexate, adriamycin, daunomycin, taxol (i.e., paclitaxel), taxol derivative (e.g., docetaxel, taxane), and mixtures thereof.

In an additional embodiment of the second aspect of the present invention, the polypeptide or polypeptide analog may be used with a pharmaceutically acceptable carrier.

In a further embodiment of the second aspect of the present invention the polypeptide or polypeptide analog may be used with a time-release means such as, for example, liposomes and polysaccharides for effecting continual dosing of said polypeptide or polypeptide analog.

It other embodiments of the second aspect of the present invention, the polypeptide or polypeptide analog may be used with an anticancer drug and a pharmaceutically acceptable carrier, with an anticancer drug and a time-release means, with a pharmaceutically acceptable carrier and a time-release means, or with an anticancer drug, a pharmaceutically acceptable and a time-release means. Some examples of an anticancer drug, a pharmaceutically acceptable carrier and a time-release means are described herein.

In a third aspect, the present invention relates to a method for treating a patient with a tumor or more precisely with prostatic

adenocarcinoma, stomach cancer, breast cancer, endometrial, ovarian or other cancers of epithelial secretion, or benign prostate hyperplasia (BPH), the method comprising administering to the patient a pharmaceutical composition comprising a polypeptide or polypeptide analog selected from the group consisting of rHuPSP94 as set forth in SEQ ID NO: 2, the decapeptide as set forth in SEQ ID NO: 3, the polypeptide as set forth in SEQ ID NO: 4 (polypeptide 7-21), the polypeptide as set forth in SEQ ID NO: 5 (PCK3145), and the polypeptide as set forth in SEQ ID NO: 6 (polypeptide 76-94), a polypeptide analog selected from the group consisting of a polypeptide analog of at least five contiguous amino acids of SEQ ID NO: 2, of SEQ ID NO: 3, of SEQ ID NO: 4, of SEQ ID NO: 5, or of SEQ ID NO: 6, a polypeptide analog of at least two contiguous amino acids of SEQ ID NO: 2, of SEQ ID NO: 3, of SEQ ID NO: 4, of SEQ ID NO: 5, or of SEQ ID NO: 6, a polypeptide analog consisting of the amino acid sequence $X_1 W Q X_2 D X_1 C X_1 X_2 C X_2 C X_3 X_1 X_2$ as set forth in SEQ ID NO: 89, wherein X_1 is either glutamic acid (Glu), asparagine (Asn) or aspartic acid (Asp), X_2 is either threonine (Thr) or serine (Ser), and X_3 is either tyrosine (Tyr) or phenylalanine (Phe), a polypeptide analog comprising SEQ ID NO: 5 and having an addition of at least one amino acid to its amino-terminus, wherein said polypeptide analog comprising SEQ ID NO: 5 is selected from the group consisting of SEQ ID NO: 59 to SEQ ID NO: 88, a polypeptide analog comprising SEQ ID NO: 5 and having an addition of at least one amino acid to its carboxy-terminus, wherein said polypeptide analog comprising SEQ ID NO: 5 is selected from the group consisting of SEQ ID NO: 10 to SEQ ID NO: 58, a polypeptide analog comprising two to fifty units of SEQ ID NO: 5, a polypeptide analog comprising two to ten units of SEQ ID NO: 5, a polypeptide analog consisting of a sequence of from two to fourteen amino acid units wherein the amino acid units are selected from the group of amino acid units of SEQ ID NO: 5 consisting of glutamic acid (Glu), tryptophan (Trp), glutamine (Gln), threonine (Thr), aspartic acid (Asp), asparagine (Asn), cysteine (Cys), or tyrosine (Tyr), a polypeptide analog having at least 90 % of its amino acid sequence identical to the amino acid sequence set forth in SEQ ID NO: 5, a polypeptide analog having at least 70 % of its amino acid sequence identical to the amino acid sequence set forth in SEQ ID NO: 5, and a polypeptide analog having at least 50 % of its amino acid sequence identical to the amino acid sequence set forth in SEQ ID NO: 5 and mixtures thereof. The polypeptide analog mentioned herein may be capable of inhibiting the growth of a tumor or more precisely may be capable of inhibiting the growth of prostatic adenocarcinoma, stomach cancer, breast cancer, endometrial, ovarian

or other cancers of epithelial secretion, or benign prostate hyperplasia (BPH).

5 The method for treating a patient as described above may result, for example, in the inhibition (e.g., reduction, control, attenuation, prohibition) of the growth of a tumor(s) in a patient suffering for example from prostatic adenocarcinoma, stomach cancer, breast cancer, endometrial, ovarian or other cancers of epithelial secretion, or benign prostate hyperplasia (BPH). The method
10 described above may be performed, for example, by administering to the patient a pharmaceutical composition comprising a polypeptide, a polypeptide analog, or mixtures thereof of the present invention.

15 In one embodiment of the third aspect of the present invention, the polypeptide or polypeptide analog may be used with an anticancer drug, such as, for example, mitomycin, idarubicin, cisplatin, 5-fluoro-uracil, methotrexate, adriamycin, daunomycin, taxol (i.e., paclitaxel), taxol derivative (e.g., docetaxel, taxane), and mixtures thereof.

20 In an additional embodiment of the third aspect of the present invention, the polypeptide or polypeptide analog may be used with a pharmaceutically acceptable carrier.

25 In a further embodiment of the third aspect of the present invention the polypeptide or polypeptide analog may be used with a time-release means such as for example, liposomes and polysaccharides for effecting continual dosing of said polypeptide or polypeptide analog.

30 It other embodiments of the third aspect of the present invention, the polypeptide or polypeptide analog may be used with an anticancer drug and a pharmaceutically acceptable carrier, with an anticancer drug and a time-release means, with a pharmaceutically acceptable carrier and a time-release means, or with an anticancer drug, a pharmaceutically acceptable and a time-release means. Some
35 examples of an anticancer drug, a pharmaceutically acceptable carrier and a time-release means are described herein.

40 In a fourth aspect, the present invention relates to a method for treating a patient with a tumor or more precisely with prostatic adenocarcinoma, stomach cancer, breast cancer, endometrial, ovarian or other cancers of epithelial secretion, or benign prostate hyperplasia (BPH), the method comprising administering to the patient

a pharmaceutical composition including a vector comprising the nucleotide sequence of SEQ ID NO: 9 and a pharmaceutically acceptable carrier or a pharmaceutical composition comprising a polynucleotide selected from the group consisting of a polynucleotide having at
5 least 10 to 285 contiguous residues of SEQ ID NO: 9, and a polynucleotide having at least 10 to 50 contiguous residues of SEQ ID NO: 9, and a pharmaceutically acceptable carrier.

In one embodiment of the fourth aspect of the present
10 invention, the vector or the polynucleotide may be used with an anticancer drug such as, for example, mitomycin, idarubicin, cisplatin, 5-fluoro-uracil, methotrexate, adriamycin, daunomycin, taxol (i.e., paclitaxel), taxol derivative (e.g., docetaxel, taxane), and mixtures thereof.

15 In an additional embodiment of the fourth aspect of the present invention, the vector or the polynucleotide may be used with a time-release means such as, for example, liposomes and polysaccharides for effecting continual dosing of said vector.

20 In further embodiment of the fourth aspect of the present invention, the vector or the polynucleotide may be used with an anticancer drug such as, for example, mitomycin, idarubicin, cisplatin, 5-fluoro-uracil, methotrexate, adriamycin, daunomycin,
25 taxol (i.e., paclitaxel), taxol derivative (e.g., docetaxel, taxane), and mixtures thereof and with a time-release means such as, for example, liposomes and polysaccharides for effecting continual dosing of said vector or polynucleotide.

30 In a fifth aspect, the present invention relates to a pharmaceutical composition for inhibiting (e.g., recuding, controlling, attenuating, prohibiting) the growth of a tumor in a patient suffering from prostatic adenocarcinoma, stomach cancer, breast cancer, endometrial, ovarian or other cancers of epithelial
35 secretion, or benign prostate hyperplasia (BPH), comprising:

a) a polypeptide or a polypeptide analog selected from the group consisting of rHuPSP94 as set forth in SEQ ID NO: 2, the decapeptide as set forth in SEQ ID NO: 3, the
40 polypeptide as set forth in SEQ ID NO: 4 (Polypeptide 7-21), the polypeptide as set forth in SEQ ID NO: 5 (PCK3145), the polypeptide as set forth in SEQ ID NO: 6 (Polypeptide 76-94), a polypeptide analog of at least five contiguous amino acids of SEQ ID NO: 2, of SEQ ID NO: 3,

of SEQ ID NO: 4, of SEQ ID NO: 5, or of SEQ ID NO: 6, a polypeptide analog of at least two contiguous amino acids of SEQ ID NO: 2, of SEQ ID NO: 3, of SEQ ID NO: 4, of SEQ ID NO: 5, or of SEQ ID NO: 6, a polypeptide analog consisting of the amino acid sequence $X_1 W Q X_2 D X_1 C X_1 X_2 C X_2 C X_3 X_1 X_2$ as set forth in SEQ ID NO: 89, wherein X_1 is either glutamic acid (Glu), asparagine (Asn) or aspartic acid (Asp), X_2 is either threonine (Thr) or serine (Ser), and X_3 is either tyrosine (Tyr) or phenylalanine (Phe), a polypeptide analog comprising SEQ ID NO: 5 and having an addition of at least one amino acid to its amino-terminus wherein said polypeptide analog comprising SEQ ID NO: 5 is selected from the group consisting of SEQ ID NO: 59 to SEQ ID NO: 88, a polypeptide analog comprising SEQ ID NO: 5 and having an addition of at least one amino acid to its carboxy-terminus, wherein said polypeptide analog comprising SEQ ID NO: 5 is selected from the group consisting of SEQ ID NO: 10 to SEQ ID NO: 58, a polypeptide analog comprising two to fifty units of SEQ ID NO: 5, a polypeptide analog comprising two to ten units of SEQ ID NO: 5, a polypeptide analog consisting of a sequence of from two to fourteen amino acid units wherein the amino acid units are selected from the group of amino acid units of SEQ ID NO: 5 consisting of glutamic acid (Glu), tryptophan (Trp), glutamine (Gln), threonine (Thr), aspartic acid (Asp), asparagine (Asn), cysteine (Cys), or tyrosine (Tyr), a polypeptide analog having at least 90 % of its amino acid sequence identical to the amino acid sequence set forth in SEQ ID NO: 5, a polypeptide analog having at least 70 % of its amino acid sequence identical to the amino acid sequence set forth in SEQ ID NO: 5, and a polypeptide analog having at least 50 % of its amino acid sequence identical to the amino acid sequence set forth in SEQ ID NO: 5, and mixture(s) thereof, and;

b) an anticancer drug such as, for example, mitomycin, idarubicin, cisplatin, 5-fluoro-uracil, methotrexate, adriamycin, daunomycin, taxol, taxol derivative, and mixtures thereof.

In one embodiment of the fifth aspect of the present invention the pharmaceutical composition may further comprise a time-release means such as, for example, liposomes and polysaccharides for effecting continual dosing of the composition.

In a sixth aspect, the present invention relates to a pharmaceutical composition for inhibiting the growth of a tumor in a patient suffering from prostatic adenocarcinoma, stomach cancer, breast cancer, endometrial, ovarian or other cancers of epithelial secretion, or benign prostate hyperplasia (BPH), comprising:

- a) a polypeptide or polypeptide analog selected from the group consisting of rHuPSP94 as set forth in SEQ ID NO: 2, the decapeptide as set forth in SEQ ID NO: 3, the polypeptide as set forth in SEQ ID NO: 4 (Polypeptide 7-21), the polypeptide as set forth in SEQ ID NO: 5 (PCK3145), the polypeptide as set forth in SEQ ID NO: 6 (Polypeptide 76-94), a polypeptide analog of at least five contiguous amino acids of SEQ ID NO: 2, of SEQ ID NO: 3, of SEQ ID NO: 4, of SEQ ID NO: 5, or of SEQ ID NO: 6, a polypeptide analog of at least two contiguous amino acids of SEQ ID NO: 2, of SEQ ID NO: 3, of SEQ ID NO: 4, of SEQ ID NO: 5, or of SEQ ID NO: 6, a polypeptide analog consisting of the amino acid sequence $X_1 W Q X_2 D X_1 C X_1 X_2 C X_2 C X_3 X_1 X_2$ as set forth in SEQ ID NO: 89, wherein X_1 is either glutamic acid (Glu), asparagine (Asn) or aspartic acid (Asp), X_2 is either threonine (Thr) or serine (Ser), and X_3 is either tyrosine (Tyr) or phenylalanine (Phe), a polypeptide analog comprising SEQ ID NO: 5 and having an addition of at least one amino acid to its amino-terminus wherein said polypeptide analog comprising SEQ ID NO: 5 is selected from the group consisting of SEQ ID NO: 59 to SEQ ID NO: 88, a polypeptide analog comprising SEQ ID NO: 5 and having an addition of at least one amino acid to its carboxy-terminus, wherein said polypeptide analog comprising SEQ ID NO: 5 is selected from the group consisting of SEQ ID NO: 10 to SEQ ID NO: 58, a polypeptide analog comprising two to fifty units of SEQ ID NO: 5, a polypeptide analog comprising two to ten units of SEQ ID NO: 5, a polypeptide analog consisting of a sequence of from two to fourteen amino acid units wherein the amino acid units are selected from the group of amino acid units of SEQ ID NO: 5 consisting of glutamic acid (Glu), tryptophan (Trp), glutamine (Gln), threonine (Thr), aspartic acid (Asp), asparagine (Asn), cysteine (Cys), or tyrosine (Tyr), a polypeptide analog having at least 90 % of its amino acid sequence identical to the amino acid sequence set forth in SEQ ID NO: 5, a

5 polypeptide analog having at least 70 % of its amino acid sequence identical to the amino acid sequence set forth in SEQ ID NO: 5, and a polypeptide analog having at least 50 % of its amino acid sequence identical to the amino acid sequence set forth in SEQ ID NO: 5, and mixture(s) thereof, and;

b) a pharmaceutically acceptable carrier.

10 In one embodiment of the sixth aspect of the present invention the pharmaceutical composition may further comprise a time-release means such as, for example, liposomes and polysaccharides for effecting continual dosing of the composition.

15 In a second embodiment of the sixth aspect of the present invention the pharmaceutical composition may further comprise an anticancer drug such as, for example, mitomycin, idarubicin, cisplatin, 5-fluoro-uracil, methotrexate, adriamycin, daunomycin, taxol, taxol derivative, and mixtures thereof.

20 In a third embodiment of the sixth aspect of the present invention, the pharmaceutical composition may further comprise a time-release means and an anticancer drug. Examples of time-release means and anticancer drug are described herein.

25 In a seventh aspect, the present invention relates to a pharmaceutical composition comprising:

30 a) A polypeptide or polypeptide analog selected from the group consisting of rHuPSP94 as set forth in SEQ ID NO: 2, the decapeptide as set forth in SEQ ID NO: 3, the polypeptide as set forth in SEQ ID NO: 4 (polypeptide 7-21), the polypeptide as set forth in SEQ ID NO: 5 (PCK3145), the polypeptide as set forth in SEQ ID NO: 6 (polypeptide 76-94), a polypeptide analog of at least five contiguous amino acids of SEQ ID NO: 2, of SEQ ID NO: 3, of SEQ ID NO: 4, of SEQ ID NO: 5, or of SEQ ID NO: 6, a polypeptide analog of at least two contiguous amino acids of SEQ ID NO: 2, of SEQ ID NO: 3, of SEQ ID NO: 4, of SEQ ID NO: 5, or of SEQ ID NO: 6, a polypeptide analog consisting of the amino acid sequence $X_1 W Q X_2 D X_1 C X_1 X_2 C X_2 C X_3 X_1 X_2$ as set forth in SEQ ID NO: 89, wherein X_1 is either glutamic acid (Glu), asparagine (Asn) or aspartic acid (Asp), X_2 is either threonine (Thr) or serine (Ser),

and X₃ is either tyrosine (Tyr) or phenylalanine (Phe), a polypeptide analog comprising SEQ ID NO: 5 and having an addition of at least one amino acid to its amino-terminus wherein said polypeptide analog comprising SEQ ID NO:5 is selected from the group consisting of SEQ ID NO: 59 to SEQ ID NO: 88, a polypeptide analog comprising SEQ ID NO: 5 and having an addition of at least one amino acid to its carboxy-terminus, wherein said polypeptide analog comprising SEQ ID NO:5 is selected from the group consisting of SEQ ID NO: 10 to SEQ ID NO: 58, a polypeptide analog comprising two to fifty units of SEQ ID NO: 5, a polypeptide analog comprising two to ten units of SEQ ID NO: 5, a polypeptide analog consisting of a sequence of from two to fourteen amino acid units wherein the amino acid units are selected from the group of amino acid units of SEQ ID NO: 5 consisting of glutamic acid (Glu), tryptophan (Trp), glutamine (Gln), threonine (Thr), aspartic acid (Asp), asparagine (Asn), cysteine (Cys), or tyrosine (Tyr), a polypeptide analog having at least 90 % of its amino acid sequence identical to the amino acid sequence set forth in SEQ ID NO: 5, a polypeptide analog having at least 70 % of its amino acid sequence identical to the amino acid sequence set forth in SEQ ID NO: 5, and a polypeptide analog having at least 50 % of its amino acid sequence identical to the amino acid sequence set forth in SEQ ID NO: 5, and mixture(s) thereof, in a therapeutically effective amount, and;

b) an anticancer drug such as, for example, mitomycin, idarubicin, cisplatin, 5-fluoro-uracil, methotrexate, adriamycin, daunomycin, taxol, taxol derivative, and mixtures thereof in a therapeutically effective amount.

In one embodiment of the seventh aspect of the present invention the pharmaceutical composition may further comprise a time-release means such as, for example, liposomes and polysaccharides for effecting continual dosing of the composition.

In an eighth aspect, the present invention relates to a pharmaceutical composition comprising:

a) a polypeptide or polypeptide analog selected from the group consisting of rHuPSP94 as set forth in SEQ ID NO: 2, the decapeptide as set forth in SEQ ID NO: 3, the polypeptide

as set forth in SEQ ID NO: 4 (polypeptide 7-21), the polypeptide as set forth in SEQ ID NO: 5 (PCK3145), the polypeptide as set forth in SEQ ID NO: 6 (polypeptide 76-94), a polypeptide analog of at least five contiguous amino acids of SEQ ID NO: 2, of SEQ ID NO: 3, of SEQ ID NO: 4, of SEQ ID NO: 5, or of SEQ ID NO: 6, a polypeptide analog of at least two contiguous amino acids of SEQ ID NO: 2, of SEQ ID NO: 3, of SEQ ID NO: 4, of SEQ ID NO: 5, or of SEQ ID NO: 6, a polypeptide analog consisting of the amino acid sequence X_1 W Q X_2 D X_1 C X_1 X_2 C X_2 C X_3 X_1 X_2 as set forth in SEQ ID NO: 89, wherein X_1 is either glutamic acid (Glu), asparagine (Asn) or aspartic acid (Asp), X_2 is either threonine (Thr) or serine (Ser), and X_3 is either tyrosine (Tyr) or phenylalanine (Phe), a polypeptide analog comprising SEQ ID NO: 5 and having an addition of at least one amino acid to its amino-terminus wherein said polypeptide analog comprising SEQ ID NO: 5 is selected from the group consisting of SEQ ID NO: 59 to SEQ ID NO: 88, a polypeptide analog comprising SEQ ID NO: 5 and having an addition of at least one amino acid to its carboxy-terminus, wherein said polypeptide analog comprising SEQ ID NO: 5 is selected from the group consisting of SEQ ID NO: 10 to SEQ ID NO: 58, a polypeptide analog comprising two to fifty units of SEQ ID NO: 5, a polypeptide analog comprising two to ten units of SEQ ID NO: 5, a polypeptide analog consisting of a sequence of from two to fourteen amino acid units wherein the amino acid units are selected from the group of amino acid units of SEQ ID NO: 5 consisting of glutamic acid (Glu), tryptophan (Trp), glutamine (Gln), threonine (Thr), aspartic acid (Asp), asparagine (Asn), cysteine (Cys), or tyrosine (Tyr), a polypeptide analog having at least 90 % of its amino acid sequence identical to the amino acid sequence set forth in SEQ ID NO: 5, a polypeptide analog having at least 70 % of its amino acid sequence identical to the amino acid sequence set forth in SEQ ID NO: 5, and a polypeptide analog having at least 50 % of its amino acid sequence identical to the amino acid sequence set forth in SEQ ID NO: 5, and mixture(s) thereof, in a therapeutically effective amount, and;

b) a pharmaceutically acceptable carrier.

In one embodiment of the eighth aspect of the present invention the pharmaceutical composition may further comprise a time-release means such as, for example, liposomes and polysaccharides for effecting continual dosing of the composition.

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In a second embodiment of the eighth aspect of the present invention, the pharmaceutical composition may further comprise an anticancer drug such as, for example, mitomycin, idarubicin, cisplatin, 5-fluoro-uracil, methotrexate, adriamycin, daunomycin, taxol, taxol derivative, and mixtures thereof.

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In a third embodiment of the eighth aspect of the present invention, the pharmaceutical composition may further comprise a time-release means and an anticancer drug. Examples of time-release means and anticancer drug are described herein.

15

In a ninth aspect, the present invention relates to a pharmaceutical composition for inhibiting (reducing, controlling, attenuating, prohibiting) the growth of a tumor in a patient suffering from prostatic adenocarcinoma, stomach cancer, breast cancer, endometrial, ovarian or other cancers of epithelial secretion, or benign prostate hyperplasia (BPH), comprising a vector comprising the nucleotide sequence of SEQ ID NO: 9 and a pharmaceutically acceptable carrier, or a polynucleotide selected from the group consisting of a polynucleotide having at least 10 to 285 contiguous residues of SEQ ID NO: 9 and a polynucleotide having at least 10 to 50 contiguous residues of SEQ ID NO: 9, and a pharmaceutically acceptable carrier.

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In one embodiment of the ninth aspect of the present invention, the pharmaceutical composition may further comprise an anticancer drug such as, for example, mitomycin, idarubicin, cisplatin, 5-fluoro-uracil, methotrexate, adriamycin, daunomycin, taxol (i.e., paclitaxel), taxol derivative (e.g., docetaxel, taxane), and mixtures thereof.

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In a tenth aspect, the present invention relates to a pharmaceutical composition for inhibiting the growth of a tumor in a patient, comprising a vector comprising the nucleotide sequence of SEQ ID NO: 9 and a pharmaceutically acceptable carrier, or a polynucleotide selected from the group consisting of a polynucleotide having at least 10 to 285 contiguous residues of SEQ ID NO: 9 and a polynucleotide having at least 10 to 50 contiguous residues of SEQ ID NO: 9, and a pharmaceutically acceptable carrier.

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In one embodiment of the tenth aspect of the present invention, the pharmaceutical composition may further comprise an anticancer drug such as, for example, mitomycin, idarubicin, cisplatin, 5-fluoro-uracil, methotrexate, adriamycin, daunomycin, taxol (i.e., paclitaxel), taxol derivative (e.g., docetaxel, taxane), and mixtures thereof.

In an eleventh aspect, the present invention relates to a method for treating patients with a disease characterized by elevated levels of FSH comprising administering a pharmaceutical composition in an appropriate dosage form, the pharmaceutical composition comprising a polypeptide or polypeptide analog selected from the group consisting of rHuPSP94 as set forth SEQ ID NO: 2, the decapeptide as set forth in SEQ ID NO: 3, the polypeptide as set forth in SEQ ID NO: 4, the polypeptide as set forth in SEQ ID NO: 5, and the polypeptide as set forth in SEQ ID NO: 6, a polypeptide analog of at least five contiguous amino acids of SEQ ID NO: 2, of SEQ ID NO: 3, of SEQ ID NO: 4, of SEQ ID NO: 5, or of SEQ ID NO: 6, a polypeptide analog of at least two contiguous amino acids of SEQ ID NO: 2, of SEQ ID NO: 3, of SEQ ID NO: 4, of SEQ ID NO: 5, or of SEQ ID NO: 6, a polypeptide analog consisting of the amino acid sequence $X_1 W Q X_2 D X_1 C X_1 X_2 C X_2 C X_3 X_1 X_2$ as set forth in SEQ ID NO: 89, wherein X_1 is either glutamic acid (Glu), asparagine (Asn) or aspartic acid (Asp), X_2 is either threonine (Thr) or serine (Ser), and X_3 is either tyrosine (Tyr) or phenylalanine (Phe), a polypeptide analog comprising SEQ ID NO: 5 and having an addition of at least one amino acid to its amino-terminus, wherein said polypeptide analog comprising SEQ ID NO: 5 is selected from the group consisting of SEQ ID NO: 59 to SEQ ID NO: 88, a polypeptide analog comprising SEQ ID NO: 5 and having an addition of at least one amino acid to its carboxy-terminus, wherein said polypeptide analog comprising SEQ ID NO: 5 is selected from the group consisting of SEQ ID NO: 10 to SEQ ID NO: 58, a polypeptide analog comprising two to fifty units of SEQ ID NO: 5, a polypeptide analog comprising two to ten units of SEQ ID NO: 5, a polypeptide analog consisting of a sequence of from two to fourteen amino acid units wherein the amino acid units are selected from the group of amino acid units of SEQ ID NO: 5 consisting of glutamic acid (Glu), tryptophan (Trp), glutamine (Gln), threonine (Thr), aspartic acid (Asp), asparagine (Asn), cysteine (Cys), or tyrosine (Tyr), a polypeptide analog having at least 90 % of its amino acid sequence identical to the amino acid sequence set forth in SEQ ID NO: 5, a polypeptide analog having at least 70 % of its amino acid sequence identical to the amino acid sequence set forth in SEQ ID NO: 5, and a polypeptide analog having at least 50 % of its amino

acid sequence identical to the amino acid sequence set forth in SEQ ID NO: 5, and mixtures thereof, and a pharmaceutically acceptable carrier in a human dose.

- 5 In a twelfth aspect, the present invention relates to the use of a polypeptide or a polypeptide analog selected from the group consisting of rHuPSP94 as set forth in SEQ ID NO: 2, the decapeptide as set forth in SEQ ID NO: 3, the polypeptide as set forth in SEQ ID NO: 4 (polypeptide 7-21), the polypeptide as set forth in SEQ ID NO: 5 (PCK3145), and the polypeptide as set forth in SEQ ID NO: 6 (polypeptide 76-94), a polypeptide analog of at least five contiguous amino acids of SEQ ID NO: 2, of SEQ ID NO: 3, of SEQ ID NO: 4, of SEQ ID NO: 5, or of SEQ ID NO: 6, a polypeptide analog of at least two contiguous amino acids of SEQ ID NO: 2, of SEQ ID NO: 3, of SEQ ID NO: 4, of SEQ ID NO: 5, or of SEQ ID NO: 6, a polypeptide analog consisting of the amino acid sequence $X_1 W Q X_2 D X_1 C X_1 X_2 C X_2 C X_3 X_1 X_2$ as set forth in SEQ ID NO: 89, wherein X_1 is either glutamic acid (Glu), asparagine (Asn) or aspartic acid (Asp), X_2 is either threonine (Thr) or serine (Ser), and X_3 is either tyrosine (Tyr) or phenylalanine (Phe), a polypeptide analog comprising SEQ ID NO: 5 and having an addition of at least one amino acid to its amino-terminus, wherein said polypeptide analog comprising SEQ ID NO: 5 is selected from the group consisting of SEQ ID NO: 59 to SEQ ID NO: 88, a polypeptide analog comprising SEQ ID NO: 5 and having an addition of at least one amino acid to its carboxy-terminus, wherein said polypeptide analog comprising SEQ ID NO: 5 is selected from the group consisting of SEQ ID NO: 10 to SEQ ID NO: 58, a polypeptide analog comprising two to fifty units of SEQ ID NO: 5, a polypeptide analog comprising two to ten units of SEQ ID NO: 5, a polypeptide analog consisting of a sequence of from two to fourteen amino acid units wherein the amino acid units are selected from the group of amino acid units of SEQ ID NO: 5 consisting of glutamic acid (Glu), tryptophan (Trp), glutamine (Gln), threonine (Thr), aspartic acid (Asp), asparagine (Asn), cysteine (Cys), or tyrosine (Tyr), a polypeptide analog having at least 90 % of its amino acid sequence identical to the amino acid sequence set forth in SEQ ID NO: 5, a polypeptide analog having at least 70 % of its amino acid sequence identical to the amino acid sequence set forth in SEQ ID NO: 5, and a polypeptide analog having at least 50 % of its amino acid sequence identical to the amino acid sequence set forth in SEQ ID NO: 5 and mixture(s) thereof, for treating patients with a disease characterized by elevated levels of FSH.

The use of a polypeptide or a polypeptide analog selected from the group consisting of rHuPSP94 as set forth in SEQ ID NO: 2, the decapeptide as set forth in SEQ ID NO: 3, the polypeptide as set forth in SEQ ID NO: 4 (polypeptide 7-21), the polypeptide as set forth in SEQ ID NO: 5 (PCK3145), the polypeptide as set forth in SEQ ID NO: 6 (polypeptide 76-94), a polypeptide analog of at least five contiguous amino acids of SEQ ID NO: 2, of SEQ ID NO: 3, of SEQ ID NO: 4, of SEQ ID NO: 5, or of SEQ ID NO: 6, a polypeptide analog of at least two contiguous amino acids of SEQ ID NO: 2, of SEQ ID NO: 3, of SEQ ID NO: 4, of SEQ ID NO: 5, or of SEQ ID NO: 6, a polypeptide analog consisting of the amino acid sequence $X_1 W Q X_2 D X_1 C X_1 X_2 C X_2 C X_3 X_1 X_2$ as set forth in SEQ ID NO: 89, wherein X_1 is either glutamic acid (Glu), asparagine (Asn) or aspartic acid (Asp), X_2 is either threonine (Thr) or serine (Ser), and X_3 is either tyrosine (Tyr) or phenylalanine (Phe), a polypeptide analog comprising SEQ ID NO: 5 and having an addition of at least one amino acid to its amino-terminus, wherein said polypeptide analog comprising SEQ ID NO: 5 is selected from the group consisting of SEQ ID NO: 59 to SEQ ID NO: 88, a polypeptide analog comprising SEQ ID NO: 5 and having an addition of at least one amino acid to its carboxy-terminus, wherein said polypeptide analog comprising SEQ ID NO: 5 is selected from the group consisting of SEQ ID NO: 10 to SEQ ID NO: 58, a polypeptide analog comprising two to fifty units of SEQ ID NO: 5, a polypeptide analog comprising two to ten units of SEQ ID NO: 5, a polypeptide analog consisting of a sequence of from two to fourteen amino acid units wherein the amino acid units are selected from the group of amino acid units of SEQ ID NO: 5 consisting of glutamic acid (Glu), tryptophan (Trp), glutamine (Gln), threonine (Thr), aspartic acid (Asp), asparagine (Asn), cysteine (Cys), or tyrosine (Tyr), a polypeptide analog having at least 90 % of its amino acid sequence identical to the amino acid sequence set forth in SEQ ID NO: 5, a polypeptide analog having at least 70 % of its amino acid sequence identical to the amino acid sequence set forth in SEQ ID NO: 5, and a polypeptide analog having at least 50 % of its amino acid sequence identical to the amino acid sequence set forth in SEQ ID NO: 5 and mixtures thereof for the manufacture of a medicament for the therapeutic treatment of prostatic adenocarcinoma, stomach cancer, breast cancer, endometrial, ovarian or other cancers of epithelial secretion, benign prostate hyperplasia (BPH) or a disease characterized by elevated levels of FSH.

In accordance with the present invention, rHuPSP94 may be used in a dosage range from about 10 micrograms/kg/day to about 4 milligrams/kg/day, in a dosage range from about 500 picograms/kg/day

to about 1 milligram/kg/day, in a dosage range from about 5 nanograms/kg/day to about 10 micrograms/kg/day or in a dosage range from about 5 nanograms/kg/day to about 500 nanograms/kg/day.

5 In accordance with the present invention, the decapeptide as set forth in SEQ ID NO: 3, the polypeptide as set forth in SEQ ID NO: 4, the polypeptide as set forth in SEQ ID NO: 5, the polypeptide as set forth in SEQ ID NO: 6, and mixtures thereof may be used in a dosage range from about 100 nanograms/kg/day to about 4
10 milligrams/kg/day.

In accordance with the present invention, the anticancer drug may be mixed or not with a polypeptide or polypeptide analog or mixtures thereof or it may be given separately, by a different route,
15 or even in a different administration schedule (e.g., a different time or day).

In accordance with the present invention administration of the composition may be performed by any suitable routes including
20 administration by injection via the intra-muscular (IM), subcutaneous (SC), intra-dermal (ID), intra-venous (IV) or intra-peritoneal (IP) routes or administration at the mucosal membranes including the oral and nasal cavity membranes using any suitable means.

25 In accordance with the present invention, the composition may be used to treat gastrointestinal cancer.

It is known in the art that the proteins or polypeptides of the present invention may be made according to methods present in the
30 art. The polypeptides of the present invention may be prepared for example, from bacterial cell extracts, or through the use of recombinant techniques. Polypeptides of the present invention may, for example, be produced by transformation (transfection, transduction, or infection) of a host cell with all or part of a
35 rHuPSP94 (SEQ ID NO: 2), the decapeptide as set forth in SEQ ID NO: 3, the polypeptide as set forth in SEQ ID NO: 4 (polypeptide 7-21), the polypeptide as set forth in SEQ ID NO: 5 (PCK3145), and the polypeptide as set forth in SEQ ID NO: 6 (polypeptide 76-94) encoding DNA sequence in a suitable expression vehicle. Examples of suitable
40 expression vehicles comprise for example, plasmids, viral particles, artificial chromosomes and phages. The entire expression vehicle, or a part thereof, may be integrated into the host cell genome. In some circumstances, it is desirable to employ an inducible expression vector.

Any of a wide variety of expression systems may be used to provide the recombinant protein. The precise host cell used is not critical to the invention. Polypeptides of the present invention may be produced in a prokaryotic host (e.g., *E. coli* or *B. subtilis*) or in a eukaryotic host (yeast e.g., *Saccharomyces* or *Pichia Pastoris*; mammalian cells, e.g., monkey COS cells, mouse 3T3 cells (Todaro GJ and Green H., *J. Cell Biol.* 17: 299-313, 1963), Chinese Hamster Ovary cells (CHO) (Puck TT et al., *J. Exp. Med.* 108: 945-956, 1958), BHK, human kidney 293 cells (ATCC: CRL-1573), or human HeLa cells (ATCC:CCL-2); or insect cells).

In a yeast cell expression system such as *Pichia Pastoris* (*P. Pastoris*), DNA sequence encoding polypeptides of the present invention may be cloned into a suitable expression vector such as the pPIC9 vector (Invitrogen). Upon introduction of a vector containing the DNA sequence encoding all or part of the polypeptides of the present invention into the *P. Pastoris* host cells, recombination event may occur for example in the AOX1 locus. Such recombination event may place the DNA sequence of the various polypeptides of the present invention under the dependency of the AOX1 gene promoter. Successful insertion of a gene (DNA sequence) encoding polypeptides of the present invention may result in an expression of such polypeptides that is regulated and/or induced by methanol added in the growth media of the host cell (for reference see Buckholz, R.G. and Gleeson, M.A.G., *Biotechnology*, 9:1067-1072, 1991; Cregg, J.M., et al., *Biotechnology*, 11:905-910, 1993; Sreekrishna, K., et al., *J. Basic Microbiol.*, 28:265-278, 1988; Wegner, G.H., *FEMS Microbiology Reviews*, 87:279-284, 1990).

In mammalian host cells, a number of viral-based expression systems may be utilized. For example, in the event where an adenovirus is used as an expression vector for the polypeptides of the present invention, nucleic acid sequence may be ligated to an adenovirus transcription/translation control complex (e.g., the late promoter and tripartite leader sequence). This chimeric gene may be inserted into the adenovirus genome, for example, by in vitro or in vivo recombination. Insertion into a non-essential region of the viral genome (e.g., region E1 or E3) may result in a recombinant virus that is viable and capable of expressing polypeptides of the present invention in infected hosts.

Proteins and polypeptides of the present invention may also be produced by plant cells. Expression vectors such as cauliflower

mosaic virus and tobacco mosaic virus and plasmid expression vectors (e.g., Ti plasmid) may be used for the expression of polypeptides in plant cells. Such cells are available from a wide range of sources (e.g., the American Type Culture Collection, Rockland, Md.). The
5 methods of transformation or transfection and the choice of expression vehicle are of course to be chosen accordingly to the host cell selected.

In an insect cell expression system such as Autographa
10 californica nuclear polyhedrosis virus (AcNPV), which grows in Spodoptera frugiperda cells, AcNPV may be used as a vector to express foreign genes. For example, DNA sequence coding for all or part of the polypeptides of the present invention may be cloned into non-essential regions of the virus (for example the polyhedrin gene) and
15 placed under control of an AcNPV promoter, (e.g., the polyhedrin promoter). Successful insertion of a gene (i.e., DNA sequence) encoding polypeptides of the present invention may result in inactivation of the polyhedrin gene and production of non-occluded recombinant virus (i.e., virus lacking the proteinaceous coat encoded
20 by the polyhedrin gene). These recombinant viruses may be used to infect spodoptera frugiperda cells in which the inserted gene is expressed.

In addition, a host cell may be chosen for its ability to
25 modulate the expression of the inserted sequences, or to modify or process the gene product in a specific, desired fashion. Such modifications (e.g., glycosylation) and processing (e.g., cleavage) of protein products may be important for the function of the protein. Different host cells have characteristics and specific mechanisms for
30 posttranslational processing and modification of proteins and gene products. Of course, cell lines or host systems may be chosen to ensure desired modification and processing of the foreign protein expressed. To this end, eukaryotic host cells that possess the cellular machinery for proper processing of the primary transcript,
35 glycosylation, and phosphorylation of the gene product may be used. Such mammalian host cells comprise for example, but are not limited to, CHO, VERO, BHK, HeLa, COS, MDCK, 293, and 3T3.

Alternatively, polypeptides of the present invention may be
40 produced by a stably transfected mammalian cell line. A number of vectors suitable for stable transfection of mammalian cells are available to the public; methods for constructing such cell lines are also publicly available. In one example, cDNA encoding the rHuPSP94 protein may be cloned into an expression vector that includes the

5 dihydrofolate reductase (DHFR) gene. Integration of the plasmid and, therefore, DNA sequence of polypeptides of the present invention, into the host cell chromosome may be selected for by including methotrexate in the cell culture media. This selection may be accomplished in most cell types.

10 Specific initiation signals may also be required for the efficient translation of DNA sequences inserted in a suitable expression vehicle as described above. These signals may include the ATG initiation codon and adjacent sequences. For example, in the event where gene or cDNA encoding polypeptides of the present invention, would not have their own initiation codon and adjacent sequences, additional translational control signals may be needed. For example, exogenous translational control signals, including, 15 perhaps, the ATG initiation codon, may be needed. It is known in the art that the initiation codon must be in phase with the reading frame of the polypeptide sequence to ensure proper translation of the desired polypeptide. Exogenous translational control signals and initiation codons may be of a variety of origins, including both 20 natural and synthetic. The efficiency of expression may be enhanced by the inclusion of appropriate transcription enhancer elements, transcription terminators.

25 As may be appreciated, a number of modifications may be made to the polypeptides and fragments of the present invention without deleteriously affecting the biological activity of the polypeptides or fragments. Polypeptides of the present invention comprises for example, those containing amino acid sequences modified either by natural processes, such as posttranslational processing, or by 30 chemical modification techniques which are known in the art. Modifications may occur anywhere in a polypeptide including the polypeptide backbone, the amino acid side-chains and the amino or carboxy termini. It will be appreciated that the same type of modification may be present in the same or varying degrees at several 35 sites in a given polypeptide. Also, a given polypeptide may contain many types of modifications. Polypeptides may be branched as a result of ubiquitination, and they may be cyclic, with or without branching. Cyclic, branched and branched cyclic polypeptides may result from posttranslational natural processes or may be made by 40 synthetic methods. Modifications comprise for example, without limitation, acetylation, acylation, addition of acetomidomethyl (Acm) group, ADP-ribosylation, amidation, covalent attachment to flavin, covalent attachment to a heme moiety, covalent attachment of a nucleotide or nucleotide derivative, covalent attachment of a lipid

or lipid derivative, covalent attachment of phosphatidylinositol, cross-linking, cyclization, disulfide bond formation, demethylation, formation of covalent cross-links, formation of cystine, formation of pyroglutamate, formylation, gamma-carboxylation, glycosylation, GPI anchor formation, hydroxylation, iodination, methylation, myristoylation, oxidation, proteolytic processing, phosphorylation, prenylation, racemization, selenoylation, sulfation, transfer-RNA mediated addition of amino acids to proteins such as arginylation and ubiquitination (for reference see, Protein-structure and molecular properties, 2nd Ed., T.E. Creighton, W.H. Freeman and Company, New-York, 1993).

Other type of polypeptide modification may comprises for example, amino acid insertion (i.e., addition), deletion and substitution (i.e., replacement), either conservative or non-conservative (e.g., D-amino acids, desamino acids) in the polypeptide sequence where such changes do not substantially alter the overall biological activity of the polypeptide. Polypeptides of the present invention comprise for example, biologically active mutants, variants, fragments, chimeras, and analogs; fragments encompass amino acid sequences having truncations of one or more amino acids, wherein the truncation may originate from the amino terminus (N-terminus), carboxy terminus (C-terminus), or from the interior of the protein. Analogs of the invention involve an insertion or a substitution of one or more amino acids. Variants, mutants, fragments, chimeras and analogs may have the biological property of polypeptides of the present invention which is to inhibit growth of prostatic adenocarcinoma, stomach cancer, breast cancer, endometrial, ovarian or other cancers of epithelial secretion, or benign prostate hyperplasia (BPH).

Example of substitutions may be those, which are conservative (i.e., wherein a residue is replaced by another of the same general type). As is understood, naturally occurring amino acids may be sub-classified as acidic, basic, neutral and polar, or neutral and non-polar. Furthermore, three of the encoded amino acids are aromatic. It may be of use that encoded polypeptides differing from the determined polypeptide of the present invention contain substituted codons for amino acids, which are from the same group as that of the amino acid be replaced. Thus, in some cases, the basic amino acids Lys, Arg and His may be interchangeable; the acidic amino acids Asp and Glu may be interchangeable; the neutral polar amino acids Ser, Thr, Cys, Gln, and Asn may be interchangeable; the non-polar aliphatic amino acids Gly, Ala, Val, Ile, and Leu are interchangeable

but because of size Gly and Ala are more closely related and Val, Ile and Leu are more closely related to each other, and the aromatic amino acids Phe, Trp and Tyr may be interchangeable.

5 It should be further noted that if the polypeptides are made synthetically, substitutions by amino acids, which are not naturally encoded by DNA may also be made. For example, alternative residues include the omega amino acids of the formula $\text{NH}_2(\text{CH}_2)_n\text{COOH}$ wherein n is 2-6. These are neutral nonpolar amino acids, as are sarcosine, t-
10 butyl alanine, t-butyl glycine, N-methyl isoleucine, and norleucine. Phenylglycine may substitute for Trp, Tyr or Phe; citrulline and methionine sulfoxide are neutral nonpolar, cysteic acid is acidic, and ornithine is basic. Proline may be substituted with hydroxyproline and retain the conformation conferring properties.

15 It is known in the art that mutants or variants may be generated by substitutional mutagenesis and retain the biological activity of the polypeptides of the present invention. These variants have at least one amino acid residue in the protein molecule
20 removed and a different residue inserted in its place. For example, one site of interest for substitutional mutagenesis may include but are not restricted to sites identified as the active site(s), or immunological site(s). Other sites of interest may be those, for example, in which particular residues obtained from various species
25 are identical. These positions may be important for biological activity. Examples of substitutions identified as "conservative substitutions" are shown in table 1. If such substitutions result in a change not desired, then other type of substitutions, denominated "exemplary substitutions" in table 1, or as further described herein
30 in reference to amino acid classes, are introduced and the products screened.

 In some cases it may be of interest to modify the biological activity of a polypeptide by amino acid substitution, insertion, or
35 deletion. For example, modification of a polypeptide may result in an increase in the polypeptide's biological activity, may modulate its toxicity, may result in changes in bioavailability or in stability, or may modulate its immunological activity or immunological identity. Substantial modifications in function or
40 immunological identity are accomplished by selecting substitutions that differ significantly in their effect on maintaining (a) the structure of the polypeptide backbone in the area of the substitution, for example, as a sheet or helical conformation. (b) the charge or hydrophobicity of the molecule at the target site, or

(c) the bulk of the side chain. Naturally occurring residues are divided into groups based on common side chain properties:

- 5 (1) hydrophobic: norleucine, methionine (Met), Alanine (Ala),
Valine (Val), Leucine (Leu), Isoleucine (Ile)
- (2) neutral hydrophilic: Cysteine (Cys), Serine (Ser), Threonine
 (Thr)
- (3) acidic: Aspartic acid (Asp), Glutamic acid (Glu)
- 10 (4) basic: Asparagine (Asn), Glutamine (Gln), Histidine (His),
Lysine (Lys), Arginine (Arg)
- (5) residues that influence chain orientation: Glycine (Gly),
Proline (Pro); and
- (6) aromatic: Tryptophan (Trp), Tyrosine (Tyr), Phenylalanine
 (Phe)

15

Non-conservative substitutions will entail exchanging a member of one of these classes for another.

TABLE 1. Preferred amino acid substitution

Original residue	Exemplary substitution	Conservative substitution
Ala (A)	Val, Leu, Ile	Val
Arg (R)	Lys, Gln, Asn	Lys
Asn (N)	Gln, His, Lys, Arg	Gln
Asp (D)	Glu	Glu
Cys (C)	Ser	Ser
Gln (Q)	Asn	Asn
Glu (E)	Asp	Asp
Gly (G)	Pro	Pro
His (H)	Asn, Gln, Lys, Arg	Arg
Ile (I)	Leu, Val, Met, Ala, Phe, norleucine	Leu
Leu (L)	Norleucine, Ile, Val, Met, Ala, Phe	Ile
Lys (K)	Arg, Gln, Asn	Arg
Met (M)	Leu, Phe, Ile	Leu
Phe (F)	Leu, Val, Ile, Ala	Leu
Pro (P)	Gly	Gly
Ser (S)	Thr	Thr
Thr (T)	Ser	Ser
Trp (W)	Tyr	Tyr
Tyr (Y)	Trp, Phe, Thr, Ser	Phe
Val (V)	Ile, Leu, Met, Phe, Ala, norleucine	Leu

5

Example of analogs of PCK3145 (SEQ ID NO: 5) exemplified by amino acid substitutions has been illustrated below.

Position	1	5	10	15											
PCK3145	E	W	Q	T	D	N	C	E	T	C	T	C	Y	E	T
SEQ ID NO: 89	X ₁	W	Q	X ₂	D	X ₁	C	X ₁	X ₂	C	X ₂	C	X ₃	X ₁	X ₂

10

For example, X₁ could be glutamic acid (i.e., glutamate) (Glu), aspartic acid (aspartate) (Asp), or asparagine (Asn), X₂ could be threonine (Thr) or serine (Ser) and X₃ could be tyrosine (Tyr) or phenylalanine (Phe).

Amino acids sequence insertions (e.g., additions) include amino and/or carboxyl-terminal fusions ranging in length from one residues to polypeptides containing a hundred or more residues, as well as intrasequence insertions of single or multiple amino acid residues.

5 Other insertional variants include the fusion of the N- or C-terminus of the protein to a homologous or heterologous polypeptide forming a chimera. Chimeric polypeptides (i.e., chimeras, polypeptide analog) comprise sequence of the polypeptides of the present invention fused to homologous or heterologous sequence. Said homologous or
10 heterologous sequence encompass those which, when formed into a chimera with the polypeptides of the present invention retain one or more biological or immunological properties. Examples of homologous sequences fused to PCK3145 (SEQ ID NO: 5) are illustrated below (1 to 79). Such homologous sequences are derived as it is the case for
15 PCK3145, from rHuPSP94 (SEQ ID NO: 2).

- 1) EWQTDNCETCTCYETE (SEQ ID NO: 10)
- 2) EWQTDNCETCTCYETEI (SEQ ID NO: 11)
- 3) EWQTDNCETCTCYETEIS (SEQ ID NO: 12)
- 20 4) EWQTDNCETCTCYETEISC (SEQ ID NO: 13)
- 5) EWQTDNCETCTCYETEISCC (SEQ ID NO: 14)
- 6) EWQTDNCETCTCYETEISCCT (SEQ ID NO: 15)
- 7) EWQTDNCETCTCYETEISCCTL (SEQ ID NO: 16)
- 8) EWQTDNCETCTCYETEISCCTLV (SEQ ID NO: 17)
- 25 9) EWQTDNCETCTCYETEISCCTLVS (SEQ ID NO: 18)
- 10) EWQTDNCETCTCYETEISCCTLVST (SEQ ID NO: 19)
- 11) EWQTDNCETCTCYETEISCCTLVSTP (SEQ ID NO: 20)
- 12) EWQTDNCETCTCYETEISCCTLVSTPV (SEQ ID NO: 21)
- 13) EWQTDNCETCTCYETEISCCTLVSTPVG (SEQ ID NO: 22)
- 30 14) EWQTDNCETCTCYETEISCCTLVSTPVG Y (SEQ ID NO: 23)
- 15) EWQTDNCETCTCYETEISCCTLVSTPVG YD (SEQ ID NO: 24)
- 16) EWQTDNCETCTCYETEISCCTLVSTPVG YDK (SEQ ID NO: 25)
- 17) EWQTDNCETCTCYETEISCCTLVSTPVG YDKD (SEQ ID NO: 26)
- 18) EWQTDNCETCTCYETEISCCTLVSTPVG YDKDN (SEQ ID NO: 27)
- 35 19) EWQTDNCETCTCYETEISCCTLVSTPVG YDKDNC (SEQ ID NO: 28)
- 20) EWQTDNCETCTCYETEISCCTLVSTPVG YDKDNCQ (SEQ ID NO: 29)
- 21) EWQTDNCETCTCYETEISCCTLVSTPVG YDKDNCQR (SEQ ID NO: 30)
- 22) EWQTDNCETCTCYETEISCCTLVSTPVG YDKDNCQR I (SEQ ID NO: 31)
- 23) EWQTDNCETCTCYETEISCCTLVSTPVG YDKDNCQR IF (SEQ ID NO: 32)
- 40 24) EWQTDNCETCTCYETEISCCTLVSTPVG YDKDNCQR IFK (SEQ ID NO: 33)

25) EWQTDNCETCTCYETEISCCTLVSTPVGYDKDNCQRIFKK (SEQ ID NO: 34)
 26) EWQTDNCETCTCYETEISCCTLVSTPVGYDKDNCQRIFKKE (SEQ ID NO: 35)
 27) EWQTDNCETCTCYETEISCCTLVSTPVGYDKDNCQRIFKKED (SEQ ID NO: 36)
 28) EWQTDNCETCTCYETEISCCTLVSTPVGYDKDNCQRIFKKEDC (SEQ ID NO: 37)
 5 29) EWQTDNCETCTCYETEISCCTLVSTPVGYDKDNCQRIFKKEDCK (SEQ ID NO: 38)
 30) EWQTDNCETCTCYETEISCCTLVSTPVGYDKDNCQRIFKKEDCKY (SEQ ID NO: 39)
 31) EWQTDNCETCTCYETEISCCTLVSTPVGYDKDNCQRIFKKEDCKYI (SEQ ID NO: 40)
 32) EWQTDNCETCTCYETEISCCTLVSTPVGYDKDNCQRIFKKEDCKYIV
 (SEQ ID NO: 41)
 10 33) EWQTDNCETCTCYETEISCCTLVSTPVGYDKDNCQRIFKKEDCKYIVV
 (SEQ ID NO: 42)
 34) EWQTDNCETCTCYETEISCCTLVSTPVGYDKDNCQRIFKKEDCKYIVVE
 (SEQ ID NO: 43)
 35) EWQTDNCETCTCYETEISCCTLVSTPVGYDKDNCQRIFKKEDCKYIVVEK
 15 (SEQ ID NO: 44)
 36) EWQTDNCETCTCYETEISCCTLVSTPVGYDKDNCQRIFKKEDCKYIVVEKK
 (SEQ ID NO: 45)
 37) EWQTDNCETCTCYETEISCCTLVSTPVGYDKDNCQRIFKKEDCKYIVVEKKD
 (SEQ ID NO: 46)
 20 38) EWQTDNCETCTCYETEISCCTLVSTPVGYDKDNCQRIFKKEDCKYIVVEKKDP
 (SEQ ID NO: 47)
 39) EWQTDNCETCTCYETEISCCTLVSTPVGYDKDNCQRIFKKEDCKYIVVEKKDPK
 (SEQ ID NO: 48)
 40) EWQTDNCETCTCYETEISCCTLVSTPVGYDKDNCQRIFKKEDCKYIVVEKKDPKK
 25 (SEQ ID NO: 49)
 41) EWQTDNCETCTCYETEISCCTLVSTPVGYDKDNCQRIFKKEDCKYIVVEKKDPKKT
 (SEQ ID NO: 50)
 42) EWQTDNCETCTCYETEISCCTLVSTPVGYDKDNCQRIFKKEDCKYIVVEKKDPKKT
 (SEQ ID NO: 51)
 30 43) EWQTDNCETCTCYETEISCCTLVSTPVGYDKDNCQRIFKKEDCKYIVVEKKDPKKTCS
 (SEQ ID NO: 52)
 44) EWQTDNCETCTCYETEISCCTLVSTPVGYDKDNCQRIFKKEDCKYIVVEKKDPKKT
 CSV (SEQ ID NO: 53)
 45) EWQTDNCETCTCYETEISCCTLVSTPVGYDKDNCQRIFKKEDCKYIVVEKKDPKKT
 CSVS (SEQ ID NO: 54)
 35 46) EWQTDNCETCTCYETEISCCTLVSTPVGYDKDNCQRIFKKEDCKYIVVEKKDPKKT
 CSVSE (SEQ ID NO: 55)
 47) EWQTDNCETCTCYETEISCCTLVSTPVGYDKDNCQRIFKKEDCKYIVVEKKDPKKT
 CSVSEW (SEQ ID NO: 56)

- 48) EWQTDNCETCTCYETEISCTLVSTPVG YDKDNCQRIFKKEDCKYIVVEKKDPKKT
CSVSEWI (SEQ ID NO: 57)
- 49) EWQTDNCETCTCYETEISCTLVSTPVG YDKDNCQRIFKKEDCKYIVVEKKDPKKT
CSVSEWII (SEQ ID NO: 58)
- 5 50) SCYFIPNEGVP GDSTRKCMDLKGNKHPINSEWQTDNCETCTCYET (SEQ ID NO: 88)
51) CYFIPNEGVP GDSTRKCMDLKGNKHPINSEWQTDNCETCTCYET (SEQ ID NO: 87)
52) YFIPNEGVP GDSTRKCMDLKGNKHPINSEWQTDNCETCTCYET (SEQ ID NO: 86)
53) FIPNEGVP GDSTRKCMDLKGNKHPINSEWQTDNCETCTCYET (SEQ ID NO: 85)
54) IPNEGVP GDSTRKCMDLKGNKHPINSEWQTDNCETCTCYET (SEQ ID NO: 84)
- 10 55) PNEGVP GDSTRKCMDLKGNKHPINSEWQTDNCETCTCYET (SEQ ID NO: 83)
56) NEGVP GDSTRKCMDLKGNKHPINSEWQTDNCETCTCYET (SEQ ID NO: 82)
57) EGVP GDSTRKCMDLKGNKHPINSEWQTDNCETCTCYET (SEQ ID NO: 81)
58) GVP GDSTRKCMDLKGNKHPINSEWQTDNCETCTCYET (SEQ ID NO: 80)
59) VPGDSTRKCMDLKGNKHPINSEWQTDNCETCTCYET (SEQ ID NO: 79)
- 15 60) PGDSTRKCMDLKGNKHPINSEWQTDNCETCTCYET (SEQ ID NO: 78)
61) GDSTRKCMDLKGNKHPINSEWQTDNCETCTCYET (SEQ ID NO: 77)
62) DSTRKCMDLKGNKHPINSEWQTDNCETCTCYET (SEQ ID NO: 76)
63) STRKCMDLKGNKHPINSEWQTDNCETCTCYET (SEQ ID NO: 75)
64) TRKCMDLKGNKHPINSEWQTDNCETCTCYET (SEQ ID NO: 74)
- 20 65) RKCMDLKGNKHPINSEWQTDNCETCTCYET (SEQ ID NO: 73)
66) KCMDLKGNKHPINSEWQTDNCETCTCYET (SEQ ID NO: 72)
67) CMDLKGNKHPINSEWQTDNCETCTCYET (SEQ ID NO: 71)
68) MDLKGNKHPINSEWQTDNCETCTCYET (SEQ ID NO: 70)
69) DLKGNKHPINSEWQTDNCETCTCYET (SEQ ID NO: 69)
- 25 70) LKGNKHPINSEWQTDNCETCTCYET (SEQ ID NO: 68)
71) KGNKHPINSEWQTDNCETCTCYET (SEQ ID NO: 67)
72) GNKHPINSEWQTDNCETCTCYET (SEQ ID NO: 66)
73) NKHPINSEWQTDNCETCTCYET (SEQ ID NO: 65)
74) KHPINSEWQTDNCETCTCYET (SEQ ID NO: 64)
- 30 75) HPINSEWQTDNCETCTCYET (SEQ ID NO: 63)
76) PINSEWQTDNCETCTCYET (SEQ ID NO: 62)
77) INSEWQTDNCETCTCYET (SEQ ID NO: 61)
78) NSEWQTDNCETCTCYET (SEQ ID NO: 60)
79) SEWQTDNCETCTCYET (SEQ ID NO: 59)
- 35

Other type of chimera generated by homologous fusion includes new polypeptides formed by the repetition of two or more polypeptides of the present invention. The number of repeat may be, for example, between 2 and 50 units (i.e., repeats). In some instance, it may be

useful to have a new polypeptide with a number of repeat greater than 50. Examples of new polypeptides formed by the repetition of PCK3145 (SEQ ID NO: 5) are illustrated below (80 to 82). In some instance, SEQ ID NO: 5 units may be separated by a linker or an adaptor of variable length.

80) EWQTDNCETCTCYETEEWQTDNCETCTCYETE (SEQ ID NO: 90)

81) EWQTDNCETCTCYETEEWQTDNCETCTCYETEEWQTDNCETCTCYETE (SEQ ID NO: 91)

10 82) EWQTDNCETCTCYETEEWQTDNCETCTCYETEEWQTDNCETCTCYETEEWQTDNCE
TCTCYETE (SEQ ID NO: 92)

Heterologous fusion includes new polypeptides made by the fusion of polypeptides of the present invention with heterologous polypeptides. Such polypeptides may include but are not limited to bacterial polypeptides (e.g., betalactamase, glutathione-S-transferase, or an enzyme encoded by the E.coli trp locus), yeast protein, viral proteins, phage proteins, bovine serum albumin, chemotactic polypeptides, immunoglobulin constant region (or other immunoglobulin regions), albumin, or ferritin.

Other type of polypeptide modification includes amino acids sequence deletions (e.g., truncations). Those generally range from about 1 to 30 residues, more preferably about 1 to 10 residues and typically about 1 to 5 residues.

A host cell transformed or transfected with nucleic acids encoding the polypeptides of the present invention (i.e., vector containing the DNA sequence of the polypeptides of the present invention) or chimeric proteins formed with the polypeptides of the present invention are also encompassed by the invention. Any host cell, which produces a polypeptide analog, mutant, variant, fragment, or chimera having at least one of the biological properties of the present invention is encompassed by the present invention. For example, such host cell may include bacterial, yeast, plant, insect or mammalian cells. In addition, the polypeptides of the present invention may be produced in transgenic animals. Transformed or transfected host cells and transgenic animals may be obtained using materials and methods that are routinely available to one skilled in the art.

DEFINITIONS

General Molecular Biology

5 Unless otherwise indicated, the recombinant DNA techniques utilized in the present invention are standard procedures, known to those skilled in the art. Example of such techniques are explained in the literature in sources such as J. Perbal, A Practical Guide to Molecular Cloning, John Wiley and Sons (1984), J. Sambrook et al ., 10 Molecular Cloning: A Laboratory Manual, Cold Spring Harbor Laboratory Press (1989), T.A. Brown (editor), Essential Molecular Biology: A Practical Approach, Volumes 1 and 2, IRL Press (1991), D.M. Glover and B.D. Hames (editors), DNA Cloning: A Practical Approach, Volumes 1-4, IRL Press (1995 and 1996), and F.M. Ausubel et al. (editors), 15 Current Protocols in Molecular Biology, Greene Pub. Associates and Wiley-Interscience (1988, including all updates until present) and are incorporated herein by reference.

20 "Polynucleotide" generally refers to any polyribonucleotide or polydeoxyribonucleotide, which may be unmodified RNA or DNA, or modified RNA or DNA. "Polynucleotides" include, without limitation single- and double-stranded DNA, DNA that is a mixture of single- and double-stranded regions, single- and double-stranded RNA, and RNA that is a mixture of single- and double-stranded regions, hybrid 25 molecules comprising DNA and RNA that may be single-stranded or, more typically, double-stranded or a mixture of single- and double-stranded regions. In addition, "polynucleotide" refers to triple-stranded regions comprising RNA or DNA or both RNA and DNA. The term polynucleotide also includes DNAs or RNAs containing one or more 30 modified bases and DNAs or RNAs with backbones modified for stability or for other reasons. "Modified" bases include, for example, tritylated bases and unusual bases such as inosine. A variety of modifications has been made to DNA and RNA; thus "polynucleotide" embraces chemically, enzymatically or metabolically modified forms of 35 polynucleotides as typically found in nature, as well as the chemical forms of DNA and RNA characteristic of viruses and cells. "Polynucleotide" includes but is not limited to linear and end-closed molecules. "Polynucleotide" also embraces relatively short polynucleotides, often referred to as oligonucleotides.

40

"Polypeptides" refers to any peptide or protein comprising two or more amino acids joined to each other by peptide bonds or modified peptide bonds (i.e., peptide isosteres). "Polypeptide" refers to both short chains, commonly referred as peptides, oligopeptides or

oligomers, and to longer chains generally referred to as proteins. As described above, polypeptides may contain amino acids other than the 20 gene-encoded amino acids.

5 As used herein the term "polypeptide analog" relates to mutants, variants, chimeras, fusions, deletions, additions and any other type of modifications made relative to a given polypeptide.

10 As used herein, the term "homologous" sequence relates to nucleotide or amino acid sequence derived from the rHuPSP94 DNA sequence or polypeptide.

15 As used herein, the term "heterologous" sequence relates to DNA sequence or amino acid sequence of a heterologous polypeptide and includes sequence other than that of PSP94.

20 As used herein, the term "tumor" relates to solid or non-solid tumors, metastatic or non-metastatic tumors, tumors of different tissue origin including, but not limited to, tumors originating in the liver, lung, brain, lymph node, bone marrow, adrenal gland, breast, colon, pancreas, prostate, stomach, or reproductive tract (cervix, ovaries, endometrium etc.). The term "tumor" as used herein, refers also to all neoplastic cell growth and proliferation, whether malignant or benign, and all pre-cancerous and cancerous cells and
25 tissues.

30 As used herein, the term "polysaccharide" refers to a substance made of two or more saccharide unit and comprise, for example, chitosan, pectin, chondroitin sulfate, cyclodextrin, dextrans, guar gum, inulin, amylose, and locust bean gum.

35 As used herein, the term "vector" refers to an autonomously replicating DNA or RNA molecule into which foreign DNA or RNA fragments are inserted and then propagated in a host cell for either expression or amplification of the foreign DNA or RNA molecule. The term « vector » comprises and is not limited to a plasmid (e.g., linearized or not) that can be used to transfer DNA sequences from one organism to another.

40 As used herein, the term "time-release encapsulation means" refers to controlled or sustained release obtained when a pharmaceutical composition is formulated, for example, with polysaccharides, biocompatible polymers, other polymeric matrices, capsules, microcapsules, microparticles, bolus preparations, osmotic

pumps, diffusion devices, liposomes, lipospheres, dry powders, or transdermal delivery systems. Other controlled release compositions of the present invention include liquids that, upon administration to a mammal, form a solid or a gel in situ. Furthermore, the term "time-release encapsulation means" or "time-release means" comprises a class of biodegradable polymers useful in achieving controlled release of a drug, for example, polylactic acid, polyglycolic acid, copolymers of polylactic and polyglycolic acid, polyepsilon caprolactone, polyhydroxy butyric acid, polyorthoesters, polyacetals, polydihydropyrans, polycyanoacylates, and crosslinked or amphipathic block copolymers of hydrogels.

As used herein, "pharmaceutical composition" means therapeutically effective amounts of the agent together with pharmaceutically acceptable diluents, preservatives, solubilizers, emulsifiers, adjuvant and/or carriers. A "therapeutically effective amount" as used herein refers to that amount which provides a therapeutic effect for a given condition and administration regimen. Such compositions are liquids or lyophilized or otherwise dried formulations and include diluents of various buffer content (e.g., Tris-HCl., acetate, phosphate), pH and ionic strength, additives such as albumin or gelatin to prevent absorption to surfaces, detergents (e.g., Tween 20, Tween 80, Pluronic F68, bile acid salts). Solubilizing agents (e.g., glycerol, polyethylene glycerol), anti-oxidants (e.g., ascorbic acid, sodium metabisulfite), preservatives (e.g., thimerosal, benzyl alcohol, parabens), bulking substances or tonicity modifiers (e.g., lactose, mannitol), covalent attachment of polymers such as polyethylene glycol to the protein, complexation with metal ions, or incorporation of the material into or onto particulate preparations of polymeric compounds such as polylactic acid, polyglycolic acid, hydrogels, etc, or onto liposomes, microemulsions, micelles, unilamellar or multilamellar vesicles, erythrocyte ghosts, or spheroplasts. Such compositions will influence the physical state, solubility, stability, rate of in vivo release, and rate of in vivo clearance. Controlled or sustained release compositions include formulation in lipophilic depots (e.g., fatty acids, waxes, oils). Also comprehended by the invention are particulate compositions coated with polymers (e.g., poloxamers or poloxamines). Other embodiments of the compositions of the invention incorporate particulate forms protective coatings, protease inhibitors or permeation enhancers for various routes of administration, including parenteral, pulmonary, nasal and oral routes. In one embodiment the pharmaceutical composition is administered parenterally, paracancerally, transmucosally,

transdermally, intramuscularly, intravenously, intradermally, subcutaneously, intraperitoneally, intraventricularly, intracranially and intratumorally.

- 5 Further, as used herein "pharmaceutically acceptable carrier" or "pharmaceutical carrier" are known in the art and include, but are not limited to, 0.01-0.1 M and preferably 0.05 M phosphate buffer or 0.8 % saline. Additionally, such pharmaceutically acceptable carriers may be aqueous or non-aqueous solutions, suspensions, and emulsions.
- 10 Examples of non-aqueous solvents are propylene glycol, polyethylene glycol, vegetable oils such as olive oil, and injectable organic esters such as ethyl oleate. Aqueous carriers include water, alcoholic/aqueous solutions, emulsions or suspensions, including saline and buffered media. Parenteral vehicles include sodium
- 15 chloride solution, Ringer's dextrose, dextrose and sodium chloride, lactated Ringer's or fixed oils. Intravenous vehicles include fluid and nutrient replenishers, electrolyte replenishers such as those based on Ringer's dextrose, and the like. Preservatives and other additives may also be present, such as, for example, antimicrobials,
- 20 antioxidants, collating agents, inert gases and the like.

Mutants, variants and analogs proteins

- 25 Mutant polypeptides will possess one or more mutations, which are deletions (e.g., truncations), insertions (e.g., additions), or substitutions of amino acid residues. Mutants can be either naturally occurring (that is to say, purified or isolated from a natural source) or synthetic (for example, by performing site-directed mutagenesis on the encoding DNA or made by other synthetic
- 30 methods such as chemical synthesis). It is thus apparent that the polypeptides of the invention can be either naturally occurring or recombinant (that is to say prepared from the recombinant DNA techniques).

- 35 A protein at least 50 % identical, as determined by methods known to those skilled in the art (for example, the methods described by Smith, T.F. and Waterman M.S. (1981) Ad. Appl.Math., 2:482-489, or Needleman, S.B. and Wunsch, C.D. (1970) J.Mol.Biol., 48: 443-453), to those polypeptides of the present invention are included in the
- 40 invention, as are proteins at least 70 % or 80 % and more preferably at least 90 % identical to the protein of the present invention. This will generally be over a region of at least 5, preferably at least 20 contiguous amino acids.

“Variant” as the term used herein, is a polynucleotide or polypeptide that differs from reference polynucleotide or polypeptide respectively, but retains essential properties. A typical variant of a polynucleotide differs in nucleotide sequence from another, reference polynucleotide. Changes in the nucleotide sequence of the variant may or may not alter the amino acid sequence of a polypeptide encoded by the reference polynucleotide. Nucleotide changes may result in amino acid substitutions, additions, deletions, fusion and truncations in the polypeptide encoded by the reference sequence, as discussed herein. A typical variant of a polypeptide differs in amino acid sequence from another, reference polypeptide. Generally, differences are limited so that the sequence of the reference polypeptide and the variant are closely similar overall and, in many regions, identical. A variant and reference polypeptide may differ in amino acid by one or more substitutions, additions, deletions, or any combination therefore. A substituted or inserted amino acid residue may or may not be one encoded by the genetic code. A variant polynucleotide or polypeptide may be a naturally occurring such as an allelic variant, or it may be a variant that is not known to occur naturally. Non-naturally occurring variants of polynucleotides and polypeptides may be made by mutagenesis techniques or by direct synthesis.

Amino acid sequence variants may be prepared by introducing appropriate nucleotide changes into DNA, or by in vitro synthesis of the desired polypeptide. Such variant include, for example, deletions, insertions, or substitutions of residues within the amino acid sequence. A combination of deletion, insertion and substitution can be made to arrive at the final construct, provided that the final protein product possesses the desired characteristics. The amino acid changes also may alter posttranslational processes such as changing the number or position of the glycosylation sites, altering the membrane anchoring characteristics, altering the intra-cellular location by inserting, deleting or otherwise affecting the transmembrane sequence of the native protein, or modifying its susceptibility to proteolytic cleavage.

It is to be understood herein, that if a “range” or “group” of substances (e.g. amino acids), substituents” or the like is mentioned or if other types of a particular characteristic (e.g. temperature, pressure, chemical structure, time, etc.) is mentioned, the present invention relates to and explicitly incorporates herein each and every specific member and combination of sub-ranges or sub-groups therein whatsoever. Thus, any specified range or group is to

be understood as a shorthand way of referring to each and every member of a range or group individually as well as each and every possible sub-ranges or sub-groups encompassed therein; and similarly with respect to any sub-ranges or sub-groups therein. Thus, for
5 example,

- 10 - with respect to a pressure greater than atmospheric, this is to be understood as specifically incorporating herein each and every individual pressure state, as well as sub-range, above atmospheric, such as for example 2 psig, 5 psig, 20 psig, 35.5 psig, 5 to 8 psig, 5 to 35, psig 10 to 25 psig, 20 to 40 psig, 35 to 50 psig, 2 to 100 psig, etc..;
- 15 - with respect to a temperature greater than 100° C, this is to be understood as specifically incorporating herein each and every individual temperature state, as well as sub-range, above 100° C, such as for example 101° C, 105° C and up, 110° C and up, 115° C and up, 110 to 135° C, 115° c to 135° C, 102° C to 150° C, up to 210° C, etc.;
- 20 - with respect to a temperature lower than 100° C, this is to be understood as specifically incorporating herein each and every individual temperature state, as well as sub-range, below 100° C, such as for example 15° C and up, 15° C to 40° C, 65° C to 95° C, 95° C and lower, etc.;
- 25 - with respect to residence or reaction time, a time of 1 minute or more is to be understood as specifically incorporating herein each and every individual time, as well
30 as sub-range, above 1 minute, such as for example 1 minute, 3 to 15 minutes, 1 minute to 20 hours, 1 to 3 hours, 16 hours, 3 hours to 20 hours etc.;
- 35 - with respect to polypeptides, a polypeptide analog consisting of at least two contiguous amino acids of a particular sequence is to be understood as specifically incorporating each and every individual possibility, such as for example, a polypeptide analog consisting of amino acid 1 and 2, a polypeptide analog consisting of amino acids 2 and
40 3, a polypeptide analog consisting of amino acids 3 and 4, a polypeptide analog consisting of amino acids 6 and 7, a polypeptide analog consisting of amino acids 9 and 10, a polypeptide analog consisting of amino acids 36 and 37, a

polypeptide analog consisting of amino acids 93 and 94, etc.

5 - with respect to polypeptides, a polypeptide analog
consisting of at least five contiguous amino acids of a
particular sequence is to be understood as specifically
incorporating each and every individual possibility, such as
for example, a polypeptide analog consisting of amino acids
1 to 5, a polypeptide analog consisting of amino acids 2 to
6, a polypeptide analog consisting of amino acids 3 to 7, a
10 polypeptide analog consisting of amino acids 6 to 10, a
polypeptide analog consisting of amino acids 9 to 13, a
polypeptide analog consisting of amino acids 36 to 40, a
polypeptide analog consisting of amino acids 90 to 94, etc.

15 - with respect to polypeptides, a polypeptide analog
comprising a particular sequence and having an addition of
at least one amino acid to its amino-terminus is to be
understood as specifically incorporating each and every
individual possibility, such as for example, a polypeptide
20 analog having an addition of one amino acid to its amino-
terminus, a polypeptide analog having an addition of two
amino acid to its amino-terminus, a polypeptide analog
having an addition of three amino acid to its amino-
terminus, a polypeptide analog having an addition of ten
25 amino acid to its amino-terminus, a polypeptide analog
having an addition of eighteen amino acid to its amino-
terminus, a polypeptide analog having an addition of forty
amino acid to its amino-terminus, a polypeptide analog
having an addition of two hundred amino acid to its amino-
30 terminus, etc.

35 - with respect to polypeptides, a polypeptide analog
comprising a particular sequence and having an addition of
at least one amino acid to its carboxy-terminus is to be
understood as specifically incorporating each and every
individual possibility, such as for example, a polypeptide
analog having an addition of one amino acid to its carboxy-
terminus, a polypeptide analog having an addition of two
amino acid to its carboxy-terminus, a polypeptide analog
40 having an addition of five amino acid to its carboxy-
terminus, a polypeptide analog having an addition of twenty
amino acid to its carboxy-terminus, a polypeptide analog
having an addition of fifty-three amino acid to its carboxy-
terminus, a polypeptide analog having an addition of three

hundred amino acid to its carboxy-terminus, etc.

5 - with respect to polypeptides, a polypeptide analog
 comprising two to fifty units of a particular sequence is to
 be understood as specifically incorporating each and every
 individual possibility, such as for example, a polypeptide
 analog comprising two units of that particular sequence, a
 polypeptide analog comprising three units of that particular
10 sequence, a polypeptide analog comprising six units of that
 particular sequence, a polypeptide analog comprising
 thirteen units of that particular sequence, a polypeptide
 analog comprising thirty-five units of that particular
 sequence, a polypeptide analog comprising fifty units of
 that particular sequence, etc.

15 - with respect to polypeptides, a polypeptide analog
 comprising two to ten units of a particular sequence is to
 be understood as specifically incorporating each and every
 individual possibility, such as for example, a polypeptide
20 analog comprising two units of that particular sequence, a
 polypeptide analog comprising three units of that particular
 sequence, a polypeptide analog comprising four units of that
 particular sequence, a polypeptide analog comprising five
 units of that particular sequence, a polypeptide analog
25 comprising six units of that particular sequence, a
 polypeptide analog comprising seven units of that particular
 sequence, a polypeptide analog comprising eight units of
 that particular sequence, a polypeptide analog comprising
 nine units of that particular sequence, and a polypeptide
30 analog comprising ten units of that particular sequence.

35 - with respect to polypeptides, a polypeptide analog
 consisting of a sequence of from two to fourteen amino acid
 units wherein the amino acid units are selected from the
 group of amino acid units of SEQ ID NO: 5 consisting of
 glutamic acid (Glu), tryptophan (Trp), glutamine (Gln),
 threonine (Thr), aspartic acid (Asp), asparagine (Asn),
 cysteine (Cys), or tyrosine (Tyr), is to be understood as
 specifically incorporating each and every individual
40 possibility, such as for example, a polypeptide analog of
 two amino acid units wherein the amino acids are
 sequentially; Glu and Trp, a polypeptide analog of two amino
 acid units wherein the amino acids are sequentially; Trp and
 Glu, a polypeptide analog of three amino acid units wherein

the amino acids are sequentially; Trp, Glu, Trp, a polypeptide analog of three amino acid units wherein the amino acids are sequentially; Trp, Trp, Trp, a polypeptide analog of three amino acid units wherein the amino acids are sequentially; Glu, Glu, Trp, a polypeptide analog of three amino acid units wherein the amino acids are, independently of the order; Tyr, Asp, Glu, a polypeptide analog of three amino acid units wherein the amino acids are, independently of the order; Thr, Asp, Asn, a polypeptide analog of three amino acid units wherein the amino acids are, independently of the order; Thr, Thr, Asn, a polypeptide analog of four amino acid units wherein the amino acids are, independently of the order; Glu, Gln, Cys, Asn, a polypeptide analog of four amino acid units wherein the amino acids are, independently of the order; Gln, Gln Cys, Trp, a polypeptide analog of four amino acid units wherein the amino acids are, Cys, Cys, Cys, Cys, a polypeptide analog of fourteen amino acid units wherein the amino acids are, independently of the order; Asn, Asp, Glu, Gln, Trp, Cys, Tyr, Thr, Thr, Asp, Asn, Gln, Thr, Cys, a polypeptide analog of fourteen amino acid units wherein the amino acids are, independently of the order; Asp, Asp, Asp, Asp, Trp, Cys, Cys, Trp, Thr, Thr, Thr, Thr, Cys, a polypeptide analog of fourteen amino acid units wherein the amino acids are, independently of the order; Tyr, Tyr, Tyr, Tyr, Tyr, Tyr, Tyr, Tyr, Tyr, Tyr, Tyr, Tyr, Tyr, Tyr, etc.

- with respect to polypeptides, a polypeptide analog having at least 90 % of its amino acid sequence identical to a particular amino acid sequence is to be understood as specifically incorporating each and every individual possibility (excluding 100 %), such as for example, a polypeptide analog having 90 % of its amino acid sequence identical to that particular amino acid sequence, a polypeptide analog having 91 % of its amino acid sequence identical to that particular amino acid sequence, a polypeptide analog having 93 % of its amino acid sequence identical to that particular amino acid sequence, a polypeptide analog having 97 % of its amino acid sequence identical to that particular amino acid sequence, a polypeptide analog having 99 % of its amino acid sequence identical to that particular amino acid sequence, etc.

- with respect to polypeptides, a polypeptide analog having at

least 70 % of its amino acid sequence identical to a particular amino acid sequence is to be understood as specifically incorporating each and every individual possibility (excluding 100 %), such as for example, a polypeptide analog having 70 % of its amino acid sequence identical to that particular amino acid sequence, a polypeptide analog having 71 % of its amino acid sequence identical to that particular amino acid sequence, a polypeptide analog having 73 % of its amino acid sequence identical to that particular amino acid sequence, a polypeptide analog having 88 % of its amino acid sequence identical to that particular amino acid sequence, a polypeptide analog having 97 % of its amino acid sequence identical to that particular amino acid sequence, a polypeptide analog having 99 % of its amino acid sequence identical to that particular amino acid sequence, etc.

- with respect to polypeptides, a polypeptide analog having at least 50 % of its amino acid sequence identical to a particular amino acid sequence is to be understood as specifically incorporating each and every individual possibility (excluding 100 %), such as for example, a polypeptide analog having 50 % of its amino acid sequence identical to that particular amino acid sequence, a polypeptide analog having 51 % of its amino acid sequence identical to that particular amino acid sequence, a polypeptide analog having 54 % of its amino acid sequence identical to that particular amino acid sequence, a polypeptide analog having 66 % of its amino acid sequence identical to that particular amino acid sequence, a polypeptide analog having 70 % of its amino acid sequence identical to that particular amino acid sequence, a polypeptide analog having 79 % of its amino acid sequence identical to that particular amino acid sequence, a polypeptide analog having 82 % of its amino acid sequence identical to that particular amino acid sequence, a polypeptide analog having 99 % of its amino acid sequence identical to that particular amino acid sequence, etc.

and similarly with respect to other parameters such as low pressures, concentrations, elements, etc...

It is also to be understood herein that "g" or "gm" is a reference to the gram weight unit; that "C" is a reference to the

Celsius temperature unit; and "psig" is a reference to "pounds per square inch gauge".

5

BRIEF DESCRIPTION OF THE DRAWINGS

Figure 1 depicts mass spectrometry analysis of polypeptide 7-21 (SEQ ID NO: 4).

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Figure 2 depicts mass spectrometry analysis of polypeptide PCK3145 (SEQ ID NO: 5).

Figure 3 depicts mass spectrometry analysis of polypeptide 76-94 (SEQ ID NO: 6).

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Figure 4a is a graph depicting the in-vitro inhibitory activity of the decapeptide of SEQ ID NO: 3 on PC-3 cells after 9 days of culture.

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Figure 4b is a graph depicting the in-vitro inhibitory activity of the native PSP94 (nPSP94) on PC-3 cells after 9 days of culture.

Figure 5a is a graph depicting the in-vitro inhibitory activity of the decapeptide of SEQ ID NO: 3 on PC-3 cells after 21 days of culture.

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Figure 5b is a graph depicting the in-vitro inhibitory activity of the native PSP94 (nPSP94) on PC-3 cells after 21 days of culture.

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Figure 6a is a graph depicting the in-vitro inhibitory activity of the decapeptide of SEQ ID NO: 3 on PC-3 cells after 10 days of culture.

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Figure 6b is a graph depicting the in-vitro inhibitory activity of the native PSP94 (nPSP94) on PC-3 cells after 10 days of culture.

Figure 7 depicts a gel showing DNA fragmentation following treatment of PC-3 cells with polypeptide PCK3145 as set forth in SEQ ID NO: 5.

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Figure 8 is a graph depicting the results of an apoptosis assay with an ELISA plus kit following polypeptide treatment of PC-3 cells for 72 hours with various concentration of polypeptide 7-21 (SEQ ID NO: 4), polypeptide PCK3145 (SEQ ID NO: 5), polypeptide 76-94 (SEQ ID NO: 6) or native PSP94 (SEQ ID NO: 1).

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Figure 9 is a graph depicting in vitro fibroblast cell growth when exposed for 72 hours to various concentration of native PSP94 (nPSP94) (SEQ ID NO: 1) or various concentration of rHuPSP94 (SEQ ID NO: 2) or polypeptide 7-21 (SEQ ID NO: 4), polypeptide PCK3145 (SEQ ID NO: 5), or polypeptide 76-94 (SEQ ID NO: 6).

Figure 10 is a graph depicting the effect of polypeptide 7-21 (SEQ ID NO: 4), polypeptide PCK3145 (SEQ ID NO: 5), polypeptide 76-94 (SEQ ID NO: 6), and polypeptide 61-75 on the in vitro growth of PC-3 cells after 72 hours.

Figure 11 is a graph depicting the effect of polypeptide 22-36 and polypeptide PCK3145 (SEQ ID NO: 5) on in vitro growth of PC-3 cells after 72 hours.

Figure 12 is a graph depicting results of study no. MLL-1 on the anti-tumor efficacy validation of rHuPSP94 (rPSP94) (SEQ ID NO: 2) against Mat Ly Lu (MLL) tumor implanted in nude mice.

Figure 13 is a graph depicting results of study no. MLL-2 on the anti-tumor efficacy validation of rHuPSP94 (rPSP94) (SEQ ID NO: 2) against Mat Ly Lu (MLL) tumor implanted in nude mice.

Figure 14 is a graph depicting tumor volume (tumor growth reduction) in rHuPSP94-treated nude mice.

Figure 15 is a graph depicting tumor volume (tumor growth reduction) in decapeptide (SEQ ID NO: 3)-treated nude mice.

Figure 16 is a graph depicting tumor volume (tumor growth reduction) in control scrambled polypeptide (PB111)-treated mice.

Figure 17 is a graph depicting tumor volume (tumor growth reduction) in native-PSP94 (nPSP94)-treated mice.

Figure 18 is a graph depicting the in vitro inhibitory activity of PCK3145 (SEQ ID NO: 5) on PC-3 cells, after a 72 hours treatment, as measured by MTS (3-(4,5-dimethylthiazol-2-yl)-5-(3-carboxymethoxyphenyl)-2-(4-sulfophenyl)-2H-tetrazolium, inner salt) assay.

Figure 19 is a graph depicting the in vitro inhibitory activity of native PSP94 (SEQ ID NO: 1) and PCK3145 (SEQ ID NO: 5) (GMP grade) on PC-3 cells, after 48 hours of treatment, as measured by MTS assay.

Figure 20 is a graph depicting the in vitro inhibitory activity of PCK3145 (SEQ ID NO: 5) (GMP grade) on PC-3 cells (ATCC), after 72 hours of treatment, as measured by the MTS assay.

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Figure 21 is a graph depicting the in vitro inhibitory activity of PCK3145 (SEQ ID NO: 5) (GMP grade) on PC-3 cells (ATCC), after a 48 or 72 hours treatment, as measured by the MTS assay.

10 Figure 22 is a graph depicting the in vitro inhibitory activity of decapeptide as set forth in SEQ ID NO: 3, polypeptide 7-21 as set forth in SEQ ID NO: 4, polypeptide PCK3145 as set forth in SEQ ID NO: 5, or polypeptide 76-94 as set forth in SEQ ID NO: 6 on PC-3 cells, measured by [³H]-Thymidine uptake assay.

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Figure 23 is a graph depicting the in vitro inhibitory activity of decapeptide as set forth in SEQ ID NO: 3, polypeptide 7-21 as set forth in SEQ ID NO: 4, polypeptide PCK3145 as set forth in SEQ ID NO: 5, or polypeptide 76-94 as set forth in SEQ ID NO: 6 on PC-3 cells, measured by [³H]-Thymidine uptake assay.

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Figure 24 is a graph depicting the in vitro inhibitory activity of native PSP94 (SEQ ID NO: 1) on PC-3 cells after 72 hours treatment, measured by [³H]-Thymidine uptake assay.

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Figure 25 depicts a gel showing DNA fragmentation following treatment of PC-3 cells with PCK3145 (SEQ ID NO: 5) or doxorubicin.

Figure 26 is a graph depicting the in vivo inhibitory activity of PCK3145 (SEQ ID NO: 5) (0.1 µg/kg/day and 10 µg/kg/day) against human PC-3 tumor xenografted in nude mice.

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Figure 27 is a graph depicting the in vivo inhibitory activity of PCK3145 (SEQ ID NO: 5) (10 µg/kg/day to 1000 µg/kg/day, administered either via the intra-venous or intra-peritoneal route) against human PC-3 tumor xenografted in nude mice.

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Figure 28 is a graph depicting the in vivo inhibitory activity of polypeptide 7-21 (SEQ ID NO: 4), PCK3145 (SEQ ID NO: 5) or polypeptide 76-94 (SEQ ID NO: 6), given at doses of 1 µg/kg/day or 10 µg/kg/day, in Copenhagen rats implanted with Dunning Mat Ly Lu tumors.

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Figure 29 is a graph depicting the in vivo inhibitory activity of PCK3145 (SEQ ID NO: 5) or the scrambled polypeptide given at doses of 10 µg/kg/day or 100 µg/kg/day, in Copenhagen rats implanted with Dunning Mat Ly Lu tumors.

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Figure 30 is a graph depicting tumor weight at day 18 following PCK3145 (SEQ ID NO: 5) or scrambled polypeptide treatment (10 µg/kg/day or 100 µg/kg/day), in Copenhagen rats implanted with Dunning Mat Ly Lu tumors.

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Figure 31 is a graph depicting the efficacy of PCK3145 and taxotere (i.e. docetaxel) combination treatment in Nude mice implanted with PC-3 tumor cells in tumor growth retardation.

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DETAILED DESCRIPTION OF THE INVENTION

The recombinant human rHuPSP94 expressed in yeast is non-glycosylated and has 10 cystein residues. The molecular weight of rHuPSP94 was determined to be 11.5 kDa, compared to 10.7 kDa for its native counterpart.

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Various experimental studies have been carried out in order to determine the efficacy of rHuPSP94 (SEQ ID NO: 2) relative to the native PSP94 secreted by the diseased prostate as tumor suppressive agent. Studies have also been carried out to determine the efficacy of the decapeptide as set forth in SEQ ID NO: 3, the polypeptide as set forth in SEQ ID NO: 4 (polypeptide 7-21), the polypeptide as set forth in SEQ ID NO: 5 (PCK3145), and the polypeptide as set forth in SEQ ID NO: 6 (polypeptide 76-94), as tumor suppressive agents. The tumor suppression activity of the polypeptides of the present invention has been monitored by their ability to reduce or inhibit the growth of prostatic adenocarcinoma both in-vivo and in-vitro. Those results are summarized below.

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Studies were carried out using PC-3 human prostate adenocarcinoma line, which can be maintained both in vivo as a xenograft in nude mice and in vitro as a cell line. In addition, a rat Dunning Mat LyLu prostate tumor, which is a pre-eminent animal model for the study of CaP, was also used. The Dunning tumor is a fast growing, poorly differentiated, transplantable tumor, which can be maintained both in-vivo in the Copenhagen rat and in-vitro as a cell line.

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The following examples are offered by way of illustration and not by way of limitation.

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EXAMPLE 1

PREPARATION OF rHuPSP94 (SEQ ID NO: 2) and polypeptides (SEQ ID NO: 3, SEQ ID NO: 4, SEQ ID NO: 5 and SEQ ID NO: 6)

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Recombinant HuPSP94 was cloned and expressed in *Pichia pastoris*, and then purified and characterized as follows.

Materials

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DEAE-cellulose (DE52) was purchased from Whatman (Fairfield, New-Jersey). Dialysis membranes and the electro chemiluminescence (ECL) detection kit were purchased from Biolynx Canada (Pierce Inc.). Broad-range molecular weight markers and Econo-pack columns fitted with flow adapters were purchased from Bio-Rad Labs Ltd (California). Pellicon device was purchased from Millipore (Massachusetts). Tris-HCl was obtained from ICN. MES ((2-[N-Morpholino]ethanesulfonic acid) hydrate) was obtained from Sigma. Swine anti-rabbit IgG alkaline-phosphatase conjugates was purchased from DAKO (Denmark). *Pichia Pastoris* expression Kit version G was from Invitrogen (Carlsbad, California). Non-Radioactive High Prime DIG labeling kit® was purchased from Boehringer Mannheim (Indianapolis, Indiana). The MTS (3-(4,5-dimethylthiazol-2-yl)-5-(3-carboxymethoxyphenyl)-2-(4-sulfophenyl)-2H-tetrazolium, inner salt) assays were performed using Cell Titer Aqueous Non radioactive cell proliferation assay kit from Promega (Madison, Wisconsin). MRX microtiter plate reader was from Dynex technologies (Chantilly, Virginia). Rabbit polyclonal antiserum against PSP94 was a gift from the late Dr. A. Sheth. All primers were synthesized by Procyon Biopharma Inc. London, Ontario, Canada.

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Cell line and cell culture

P. pastoris host strain GS115 (*his4*) and all *Pichia* related products were obtained from Invitrogen. PC-3 (ATCC-# CRL 1435) cell line was obtained from the American Type Cell Culture (ATCC) and maintained in OPTI MEM (minimum essential media) with 10 % fetal bovine serum (FBS). All cell culture products were obtained from GIBCO BRL.

Cloning

TA cloning vector (pCR TM 2.1) containing human PSP94 cDNA including a 20 amino acid leader sequence described previously (Baijal-Gupta, M., et. al., J. Endocrinol., 165:425-433, 2000) was used to amplify human PSP94 without its leader sequence using appropriate primers. The primers for the polymerase chain reaction (PCR) were designed to contain an EcoRI restriction sites at either end. The 5' primer used was 5'-GGG AAG AAT TCT CAT GCT ATT TCA TA-3' (SEQ ID NO: 7) and the 3' primer, 5'-TGG ATA TCT GCA GAA TTC GGC-3' (SEQ ID NO: 8). The +1 start site for PSP94 (at a Serine residue) has been underlined in the 5' primer described above.

The PCR included 1 cycle of 12 minutes at 94 °C, followed by 25 cycles of 1 minute at 94 °C, 1 minute at 55 °C, 1 minute at 72 °C and a final step of 1 cycle of 10 minutes at 72 °C. PCR amplification of the product was performed using BM ExpandTM High Fidelity PCR System. The product was run on a 1.5 % agarose gel and the appropriate PCR product was isolated using Pharmacia Sephadex Kit (Bandprep). Subcloning of the PSP94 insert was performed in pPIC9 vector (Invitrogen). The EcoRI enzyme was used for the restriction digestion of both the plasmid and the PCR products (thus removing PSP94 signal sequence) followed by ligation and transformation, using DH5 α cells. The isolated clones were selected for by ampicillin resistance and inserts were identified by restriction mappings. The constructs were sequenced (Robart's sequencing service, London, Ontario) to identify PSP94 insert with a correct sequence as well as proper orientation and reading frame.

Screening for Clones Expressing rHuPSP94

For *Pichia pastoris* transformation, the spheroplast method was used according to manufacturer's instructions (Invitrogen) using GS115 and KM71 yeast strains. Plasmid pPIC9 with or without the PSP94 insert were linearized using SalI restriction enzyme. Transformed colonies were screened and selected for their ability to produce their own histidine, hence survived on media without histidine. All GS115 transformants scored as Mut⁺, whereas all KM71 colonies, which did not grow well in the liquid culture, scored as Mut^s. Hence a number of GS115 clones were screened for production of the highest levels of rHuPSP94 expression.

About a hundred clones were selected and grown into 2 ml of culture media until an optical density at 600 nm (OD₆₀₀) of approximately 6 was reached. Total DNA was isolated for rapid dot

blot analysis in order to detect multiple integrations by Southern blot that would possibly correspond to high rHuPSP94 expressing clones. Two hundred microliters of each culture specimens were denatured and blotted (in duplicate) to a positively charged nylon membrane, placed in a dot blot apparatus. The membrane was subsequently air-dried. The membrane was soaked between two sheets of Whatman 3MM paper for 15 minutes in a solution containing 50mM ethylenediaminetetraacetic acid (EDTA), 2.5 % beta-mercaptoethanol (BME), pH 9, followed by an incubation of 24 hours at 37 °C with 1 mg/ml Zymolyase 100T, 5 minutes in 0.1 N NaOH, 1.5 M NaCl, 0.015 M sodium citrate pH 7 and two 5 minutes incubation in 2x saline-sodium citrate (SSC). Finally the membrane was baked at 80 °C for 45 minutes and exposed to ultraviolet light (UV) for 15 minutes. Human PSP94 cDNA probe was labeled with the non-radioactive High Prime DIG labeling kit® (Boehringer Mannheim) and was used for hybridization. Hybridization with digoxigenin labeled cDNA probe (25ng/μl) was done for 2 days at 42 °C in Sodium dodecyl sulfate (SDS) buffer (SDS 7 % (w/v); formamide 50 % (v/v); 5 X SSC; 50 mM sodium phosphate, pH 7.0; N-lauroyl-sarcosine 0.1 % (w/v)) and blocking reagent, CSPD® 2 % (w/v) (Boehringer Mannheim) was used as the chemiluminescence substrate. All digoxigenin (DIG) labeling procedures were performed according to the manufacturer's instruction. Detection was performed using the Hyper film-ECL product (Amersham Life Science Inc. Arlington Hts, Illinois).

The clone with the highest signal intensity was used for all flasks shaken cultures.

Optimization of the Expression of the Protein in Flask Shaken Cultures

A clone containing the PSP94 construct was selected for high expression of the protein. Colony was grown in 25ml of basal minimum growth media (BMG) until an OD600 between 2 and 6 was obtained. This clone was further amplified in Baffled Erlenmeyer flasks in a volume of 1 liter of BMG media until the OD600 reached approximately between 2.0 to 6.0. The culture was centrifuged for 15 minutes at 2500 X g and the pellet was collected. The induction phase (i.e., induction of expression of rHuPSP94) was carried out by inoculating the cell pellet in basal minimum media (BMM). Growth was performed in Baffled flasks for 6 days, as recommended by Invitrogen. The volume of BMM added varied according to the size of the pellet collected. Five milliliters of 100 % methanol were added for each liter of culture. This was performed each day, around the same time, to a final

concentration of 0.1 % of methanol. A plasmid without the PSP94 insert served as a negative control.

To determine the optimum time for harvesting rHuPSP94 secreted in the cell culture media, aliquots were taken every 24 hours for 6 days, starting from the first day of induction. Levels of rHuPSP94 protein expression were determined by measuring OD600 and by performing a 15 % SDS-PAGE (sodium dodecyl sulfate polyacrylamide gel electrophoresis) stained with Coomassie Brilliant blue or by Western blot analysis using polyclonal antibody against PSP94.

Sample Preparation

Culture supernatant of clone showing the highest rHuPSP94 expression, post-induction (e.g., after 96 hours), was centrifuged at 2500 X g for 20 minutes. The supernatant was filtered through a 0.8 µm filter and concentrated approximately 10-fold using a Pellicon unit (Millipore). The filtered supernatant was dialyzed against 0.05 mM Tris-HCl buffer, pH 8.0, using a 3500 molecular weight cut-off membrane. An aliquot of the dialyzed supernatant was analyzed by SDS-PAGE and Western blot analysis and the rest was submitted to further purification.

Culture Conditions for Fermentation

Fermentation was carried out at the Institute for Biological Sciences, National Research Council (NRC) (Ottawa, Ontario Canada), following manufacturer's instruction (Invitrogen). For example, a fermentation procedure was initiated by inoculating 7.5 liter of media with 625 ml of a starting culture. The growth phase was carried out for approximately 2 days in BMG media until the OD600 reached approximately 0.5. The induction phase was initiated by the addition of methanol (100 %), according to the manufacturer's instructions (Invitrogen). The culture was harvested after 95 hours (i.e., after induction with methanol for 67 hours). The final volume of the culture was approximately 13.5 liters.

Sample Preparation from Fermentation Culture

The large cell mass was removed by centrifugation. The cell free media collected (9 liters) was further clarified using a 0.2 µm filtration unit (Pellicon). The remaining 8.5 liters containing secreted rHuPSP94 was tested for protein expression and stored at -20 °C for further isolation and purification of the protein.

Protein Estimation

The amount of rHuPSP94 protein secreted in the culture supernatant from the flask shaken and the fermentation process was obtained based on estimates of band intensities of samples compared to band intensities of a standard curve obtained by loading known quantities of pure lyophilized PSP94 on a SDS-PAGE. The initial estimate for rHuPSP94 at each step of purification was determined by OD at 280 nm. Quantification of total protein content at the final steps of purification was done by the BCA (bicinchoninic acid) method, using bovine serum albumin (BSA) as standard.

Lyophilization

Samples of purified rHuPSP94 were dialyzed against deionized water using a 3000 molecular weight cut-off membrane and were lyophilized.

SDS-PAGE

SDS-PAGE was performed using acrylamide at a final concentration of 15 % for the separating portion of the gel and acrylamide at a final concentration of 5 % for the stacking portion of the gel. The gel contained 0.1 % SDS and was performed under reducing conditions. Broad-range molecular weight markers were used for the estimation of molecular weight of the protein. Proteins were stained with Coomassie Brilliant Blue R-250.

Western Blotting

For immunoblotting, Mini Trans-Blot Electrophoretic Transfer Cell (Bio Rad) was used with Hi bond-C super membrane (Amersham) and 85mm blotting papers. Protein samples (0.4 µg) were loaded and separated on SDS-PAGE, as described earlier. Proteins were transferred to the membrane for 2 hours at 4 °C, using transfer buffer (25 mM Tris, 192 mM Glycine, pH 8.3 and 20 % methanol) and a transfer unit set at 200 milliamperes (mAmp). Membranes were blocked overnight by incubation in 2 % (w/v) non-fat dry milk (skim milk) dissolved in tris buffer saline (TBS: 500 mM NaCl, 20 mM Tris-HCl, pH 7.5) at room temp (RT). Membranes were washed three times with TBS containing 0.02 % (v/v) Tween-20 (this buffer is named TTBS). Membranes were subsequently incubated for 2 hours at RT with anti-PSP94 antibody (1:2000 dilution) diluted in TTBS containing 2 % skim milk. Membranes were washed twice with TTBS (5 minutes each washing), and incubated at RT with a secondary antibody (i.e., swine anti-rabbit antibody HRP conjugated) (1:5000 dilution) diluted in TTBS. Membranes were washed twice with 0.02 % TTBS (5 minutes each washing). Blots were developed using the ECL detection system,

according to manufacturer's instructions, using the Super Signal Substrate, and exposed to a Hyperfilm ECL from Amersham LS for 5 to 20 seconds. Pre-stained molecular weight markers were used for molecular weight estimation.

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Purification of rHuPSP94 using DE52 Column Chromatography

Following removal of *P. pastoris* cells from the fermentation culture, supernatant was concentrated approximately ten fold, dialyzed and subjected to anion exchange chromatography. A DE52 column having a bed volume of approximately 40 ml (2.5 cm internal diameter (id) X 8 cm height(h)) was equilibrated with 0.05 M Tris-HCl, pH 8.0 (equilibrating buffer). The sample (25 ml) containing 15 to 20 mg of rHuPSP94 protein was applied to the DE52 column at a flow rate of 1 ml/minute.

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Impurities were removed from the column by washing it with 40 to 50 ml of the equilibrating buffer, and monitoring the absorbance at 280 nm. This step was followed by the addition of 100 to 150 ml of 0.05 M Tris-HCl, pH 6.5 to the column until the pH of the wash reached approximately 6.5. The column was further washed with 100 to 150 ml of 0.05 M MES-acetate buffer, pH 6.5, until the absorbance at 280nm approached zero. Finally rHuPSP94 was eluted from the column with 0.05 M MES-acetate buffer, pH 5.0. Peak fractions were characterized by absorbance at 280 nm, followed by SDS-PAGE and Western blot analysis as described above. Fractions with high absorbance at 280 nm values (0.5 to 1.8) were pooled and dialyzed against water or PBS for storage at -20 °C and/or lyophilization.

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Amino acid Composition

Amino acid analysis of the DE52 purified flask shaken culture and fermentation cultures was carried out. The Perkin Elmer Biosystems Derivatizer-Analysis system was used with Spheri-5 PTC C-18 5µ column and UV detection at OD254.

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Mass Spectral analysis

PSP94 derived polypeptides were synthesized, were found to be in accordance with the required specifications and were analyzed by Mass Spectral Analysis. Mass spectrometry analysis of polypeptide 7-21 (SEQ ID NO: 4), PCK3145 (SEQ ID NO: 5) and polypeptide 76-94 (SEQ ID NO: 6) are represented in figures 1, 2 and 3 respectively.

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Polypeptide samples were analyzed using the PerSeptive Biosystems (Framingham, MA), with Voyager-DE MALDI-TOF mass

spectrometer using 337 nm light from a nitrogen laser. About 12 to 50 scans were averaged for each analysis.

Purified samples from the flask shaken culture and fermentation culture were analyzed using the PerSeptive Biosystems (Framingham, MA), with Voyager-DE MALDI-TOF mass spectrometer using 337 nm light from a nitrogen laser. About 50 scans were averaged for each analysis. A sample from the native PSP94 was also analyzed under similar conditions for comparison.

EXAMPLE 2

IN-VITRO EFFECT OF rHuPSP94 ON PC-3 CELLS (MTS ASSAY)

The biological activity of the rHuPSP94 was determined by its growth inhibitory effect on human prostate cancer cells PC-3. Cell proliferation was monitored on PC-3 cells using the MTS/PMS (phenazine methosulfate) kit (Promega), which primarily measures mitochondrial activity of live cells. The basic principle of this method involves the fact that the mitochondrial enzymes of the live cells metabolize the MTS/PMS dyes forming a brown colored precipitate which can be measured as optical density (OD) by absorption at 490 nm in a spectrophotometer. Therefore, the OD values are proportional to the number of living cells. In addition, monitoring of cell morphology was also performed. Cell morphology would be indicative of their health status. For example, viable cells would appear adherent and spread out whereas dead cells would be in suspension in the media and would appear granular and round.

Results of in vitro effect of rHuPSP94 on PC-3 cells measured by MTS assay are summarized in table 2, below. PC-3 cells (ATCC, Lot AT06) used in these experiments were at a passage number lower or equal to 70 ($n \geq 70$). Cells were seeded in Costar 96 well cell culture flat bottom plates in RPMI supplemented media containing 50 $\mu\text{g/ml}$ of bovine serum albumin (BSA) and 0.1 μM FeSO_4 . Peptide was diluted in the same media. Cells were continuously exposed to the polypeptides of the present invention for 72 hours without changing media. Native PSP94 or rHuPSP94 concentrated two fold were directly added to wells and diluted to 1X in order to minimize cell manipulation and avoid detachment.

The evaluation of growth inhibitory effect of rHuPSP94 on PC-3 cells indicated a substantial reduction in cell numbers (i.e.,

viability) ranging from 37 % to 57 % reduction at concentrations of 80 and 120 µg/ml of rHuPSP94 respectively. This effect was observed in 3 out of 4 experiments (Table 2). Results of trypan blue exclusion test demonstrated a cell viability of 62 % at 80 µg/ml.

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TABLE 2

Experiment no.	Sample	% Viability (control = 100%) (µg/ml)			
		40	60	80	120
1	rHuPSP94	72	78	58	43
2	rHuPSP94	63	63	63	68
3	rHuPSP94	95	85	78	ND
4	rHuPSP94	100	52	62	60
5	rHuPSP94	100	98	90	52
Sample	% Viability (control = 100%) (µg/ml)				
	5	10	20	40	80
rHuPSP94	98	84	78	70	55
rHuPSP94	92	95	80	71	59
rHuPSP94	89	69	79	68	65

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EXAMPLE 3

IN-VITRO EFFECT OF rHuPSP94 ON PC-3 CELLS ([³H]-THYMIDINE UPTAKE ASSAY)

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The in vitro growth inhibition effect of rHuPSP94 was assessed using [³H]-Thymidine uptake assay. [³H]-Thymidine uptake assay involves [³H]-Thymidine incorporation into cellular DNA of actively proliferating cells. It measures the proliferative index of the cells versus the MTS assay, which quantifies the number of lived cells following treatment. Cells were seeded in Costar 96 well cell culture flat bottom plates in RPMI supplemented media containing 50 µg/ml of bovine serum albumin (BSA) and 0.1 µM FeSO₄. PC-3 cells were exposed to various concentrations of rHuPSP94 for 72 hours and during the final 16 hours of incubation cells were pulsed with 1 µCi of [³H]-Thymidine. The radioactivity in each well of the plate is counted by a beta-counter and is expressed as total counts per minutes (cpm). Results of in vitro effect of rHuPSP94 on PC-3 cells using the [³H]-Thymidine uptake assay are summarized in Table 3 and are expressed as percentage of radioactivity measured for treated-cells relative to

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the radioactivity measured for non-treated cells (for which [³H]-thymidine uptake value was set at 100 %).

Results indicated a 65 % reduction in the percentage of cells incorporating [³H]-thymidine following treatment with rHuPSP94 at a concentration of 80 µg/ml for 72hrs, compared to the non-treated control. Results of a 65 % reduction in [³H]-thymidine uptake may also be an indication of a 65 % reduction in cell proliferation.

Comparison was performed between [³H]-Thymidine uptake assay and the MTS assay, in order to evaluate their relative sensitivity. An additional plate was set aside for MTS assay and treated in parallel with the same lot (i.e., batch) of rHuPSP94 as the one used for the [³H]-thymidine uptake assay. Result obtained for the MTS assay demonstrated a 35 % reduction in cell viability (65 % cells remaining viable) following treatment with rHuPSP94 at a concentration of 80 µg/ml, indicating that the [³H]-Thymidine uptake assay, which was able to measure a 65 % reduction in cell proliferation, may be more sensitive than the MTS assay.

TABLE 3

Experiment no.	Sample	³ [H]-Thymidine Uptake (% of control) (µg/ml)				
		5	10	20	40	80
1	rHuPSP94	94	101	98	79	35
1	native PSP94	97	98	100	98	77

EXAMPLE 4 IN-VITRO EFFECT OF DECAPEPTIDE AND OTHER POLYPEPTIDE ON PC-3 CELLS

The synthetic decapeptide (SEQ ID NO: 3) has been shown herein to mimic the biological activity of native PSP94 (nPSP94) (SEQ ID NO: 1) and therefore its effect on the PC-3 cells was studied in clonogenicity assay (colony formation). Cells were seeded in Costar 96 well cell culture flat bottom plates in RPMI supplemented media containing 50 µg/ml of bovine serum albumin (BSA) and 0.1 µM FeSO₄. Clonogenicity was evaluated for PC-3 cells grown in the presence of various concentration of the decapeptide after 9 days of culture (Figure 4a). A parallel experiment was performed with various

concentration of nPSP94 using the same experimental conditions (Figure 4b). Other experiments evaluating clonogenicity was performed with the decapeptide (Figure 5a) or nPSP94 (Figure 5b) after 21 days of culture as well as after 10 days of culture (Figure 6a: Decapeptide and Figure 6b: nPSP94).

Referring to Figures 4 to 6, the decapeptide (SEQ ID NO: 3) had a similar inhibitory action as nPSP94 (SEQ ID NO: 1) on in-vitro PC-3 cells studied. Results indicated a 40 % decrease in colony number for cells incubated with the decapeptide (SEQ ID NO: 3) at a concentration of 1 µg/ml. A decrease in colony number of up to 60 % was observed for the decapeptide (SEQ ID NO: 3) at a concentration of 10 µg/ml.

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EXAMPLE 5

DNA FRAGMENTATION ASSAY

Cell apoptosis result in DNA fragmentation can be evaluated by the presence of a DNA ladder visualized when DNA is run on a 1.2 % agarose gel. DNA ladder assay (apoptosis assay) was performed following exposure of PC-3 to various concentrations of the polypeptides for 72 hours. The polypeptides that were used in this particular experiment are polypeptide 7-21 (SEQ ID NO: 4), polypeptide PCK3145 (SEQ ID NO: 5) and polypeptide 76-94 (SEQ ID NO: 6). Visualization of DNA isolated and run on 1.2 % agarose gel, demonstrated that every polypeptides tested induced a DNA laddering effect characteristic of apoptosis. This effect was especially evident following treatment with PCK3145 (SEQ ID NO: 5), which is illustrated by figure 7. Lane 1 of the gel illustrated in figure 7 represents a lambda HindIII digest standard. Lane 2 of the gel illustrated in figure 7 represents DNA laddering effect obtained for doxorubicin-treated cells. Lane 3 of the gel illustrated in figure 7 represents DNA laddering effect obtained for cells incubated with 40 µg of nPSP94. Lane 4 of the gel illustrated in figure 7 represents DNA laddering effect obtained for cells incubated with 20 µg of nPSP94. Lane 5 of the gel illustrated in figure 7 represents DNA laddering effect obtained for cells incubated with 22.5 µM of PCK3145 (SEQ ID NO: 5). Lane 6 of the gel illustrated in figure 7 represents DNA laddering effect obtained for cells incubated with 45 µM of PCK3145 (SEQ ID NO: 5).

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EXAMPLE 6
APOPTOSIS ASSAY BY ELISA PLUS

5 The three polypeptides (SEQ ID NO: 4, SEQ ID NO: 5 and SEQ ID
NO 6) and native PSP94 used here as a positive control were tested in
ELISA plus assay to measure cell death through apoptosis. Briefly,
the ELISA plus assay is a sandwich enzyme immunoassay able to measure
mono- and oligonucleosomes present in the cytoplasmic fraction of
cell lysate using two antibodies, one directed against DNA and the
10 other directed against histones. The apoptotic cell death is
characterized by activation of endogenous endonucleases (e.g.,
calcium- and magnesium-dependant), which cleave double-stranded DNA
at the most accessible internucleosomal linker region, generating
mono- and oligonucleosomes. The enrichment of mono- and
15 oligonucleosomes in the cytoplasm of the apoptotic cells is due to
the fact that DNA degradation occurs several hours before plasma
membrane breakdown.

20 Four thousand cells were seeded in Costar 96 well cell
culture flat bottom plates in RPMI supplemented media containing 50
 $\mu\text{g/ml}$ of bovine serum albumin (BSA) and $0.1 \mu\text{M}$ FeSO_4 . The PC-3 cells
were treated with various concentrations ($22.5 \mu\text{M}$ to $90 \mu\text{M}$) of
polypeptides for 72 hours. Apoptosis assay was done as per
manufacturer's instructions using the ApopTag kit (Boehringer
25 Mannheim).

Results presented in figure 8, indicate a dose dependent
increase in the apoptotic cell death effect was observed for every
polypeptides used (SEQ ID NO: 4, SEQ ID NO: 5 and SEQ ID NO 6).
30 Polypeptide PCK3145 (SEQ ID NO: 5) was more potent than the other
polypeptides at $90 \mu\text{M}$ concentration (Figure 8).

EXAMPLE 7
INHIBITION OF CELL-GROWTH BY PSP94 POLYPEPTIDES
(Figures 9 to 11)

35 Biological activity of the polypeptides as set forth in SEQ ID
NO: 4, SEQ ID NO: 5 and SEQ ID NO 6 was determined by their growth
inhibitory effect on human prostate cancer cells PC-3. Native PSP94,
40 rHuPSP94, polypeptide 22-36 and PB111 polypeptide (scrambled
polypeptide) were also included in this experiment as controls. Cell
proliferation assay was performed on either PC-3 cells or normal
fibroblasts (used here as control) using the MTS/PMS kit (Promega).

Four thousand cells (Figure 9 and 10) or three thousand (figure 11) cells were seeded in Costar 96 well cell culture flat bottom plates in RPMI supplemented media containing 50 µg/ml of bovine serum albumin (BSA) and 0.1 µM FeSO₄. In addition, monitoring of cell morphology was also performed.

Results of these experiments are shown in figures 9 to 11. No cell inhibitory effect was observed following incubation of fibroblasts with various polypeptide concentrations (from 10 to 90 µM) for 72 hours (Figure 9). However, a significant growth inhibition was observed for polypeptides as set forth in SEQ ID NO: 4 and SEQ ID NO: 6 and more importantly with polypeptide PCK3145 (SEQ ID NO: 5) (Figure 10). Another experiment was performed using PCK3145 and polypeptide 22-36 at various concentrations on PC-3 cells, grown in OPTI-MEM media. In figures 9 to 11, the percentage of growth inhibition given for treated cells is evaluated relative to non-treated control cells for which a value of 100 % cell survival is given.

EXAMPLES 8 & 9

IN-VIVO EXPERIMENTS (Figures 12 & 13)

Studies MLL-1 and MLL-2 were performed as follows; on day 0, male Copenhagen rats were injected subcutaneously with 5 x 10⁵ Mat LyLu cells per rat. These cells were derived from cultures of Mat LyLu cell line grown in RPMI media containing 10 % (v/v) of fetal calf serum in logarithmic phase of growth. Cells were harvested from the culture flasks by trypsinization, were centrifuged at 1200 rotation per minute (rpm) and washed three times with Hanks balanced salt solution (HBSS). Following washing, cells were counted and adjusted to a concentration of 5 x 10⁶ cells/ml in HBSS. A 0.1 ml volume of tumor cell inoculum containing 5 x 10⁵ cells was administered subcutaneously into the flank region of each rat. Three days after tumor cell implantation (i.e., inoculation), animals were treated daily by a subcutaneous injection of the desired polypeptide until day 13.

Experiments illustrated in figure 12 show the anti-tumor efficacy validation of rHuPSP94 against Mat LyLu (MLL) tumor implanted in nude mice (Protocol based on S. Garde et al.; The Prostate, 22: 225-233, 1993).

For study MLL-1 (Figure 12), tumor-implanted nude mice were separated in different groups, each receiving various amount of rHuPSP94 or control reagents. The different groups used in these experiments are illustrated below. Each group contained 8 mice.

Group 1: Negative control: PBS subcutaneously (s.c.)

Group 2: Positive control: Doxorubicin at 5mg/kg intraveanously (i.v.) single bolus on day 3

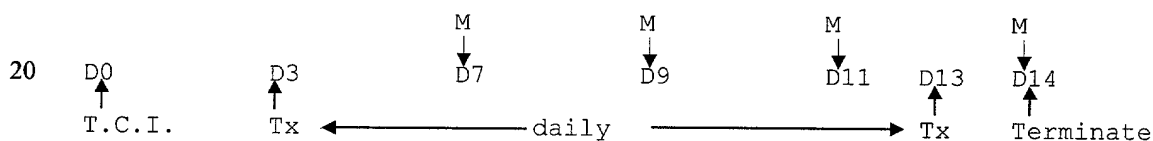
Group 3: rHuPSP94 at 1 μ g/kg/day (s.c.)

Group 4: rHuPSP94 at 10 μ g/kg/day (s.c.)

Group 5: rHuPSP94 at 100 μ g/kg/day (s.c.)

A schematic of inoculation is illustrated below;

(Tumor cell implantation (T.C.I.), treatment (Tx), measurement (M), day (D)).



Experiments illustrated in study MLL-2 show the anti-tumor efficacy validation of rHuPSP94 against Mat Ly Lu (MLL) tumor implanted in severe combined immunodeficiency (SCID) mice (Protocol based on S. Garde et al.; The Prostate, 22: 225-233, 1993).

For study MLL-2 (figure 13), tumor-implanted Scid mice were separated in different groups each receiving various amounts of rHuPSP94 or control reagents. The different groups used in these experiments are illustrated below. Each group contained 8 mice.

Group 1: Negative control: PBS (s.c.)

Group 2: Positive control: Doxorubicin at 5mg/kg i.v. single bolus on day 3

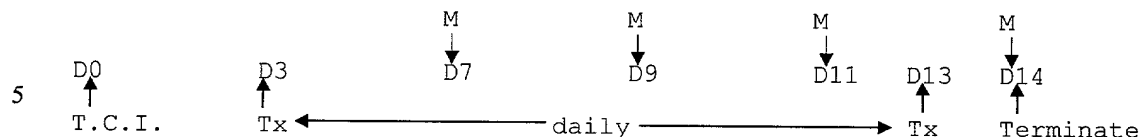
Group 3: rHuPSP94 at 1 μ g/kg/day (s.c.)

Group 4: rHuPSP94 at 10 μ g/kg/day (s.c.)

Group 5: rHuPSP94 at 100 μ g/kg/day (s.c.)

A schematic of inoculation is illustrated below;

(Tumor cell implantation (T.C.I.), treatment (Tx), measurement (M), day (D)).



10 Results of those two studies indicate a difference in tumor size and growth in Nude vs SCID mice. The tumors grew slower and were smaller in SCID mice. This may be due to some specific factors controlling tumor growth in this mouse strain. Results also show a significant tumor reduction in mice injected with Doxorubicin (positive control). For example, tumor weight reduction in Nude mice (study MLL-1) injected with Doxorubicin was 48 % (p=0.006) (p values measured by unpaired Student's t-test at p<0.05 as cut-off limit). Tumor weight reduction in SCID mice (study MLL-2) inoculated with Doxorubicin was 82 % (p=0.002) (p values measured by unpaired Student's t-test at p<0.05 as cut-off limit). Results indicate also a significant tumor reduction in mice treated with rHuPSP94 at a concentration of 1 µg/kg/day. For example, tumor weight reduction in Nude mice (study MLL-1) treated with rHuPSP94 at a concentration of 1 µg/kg/day was 26 % (p=0.042) (p values measured by unpaired Student's t-test at p<0.05 as cut-off limit). Tumor weight reduction in SCID mice (study MLL-2) treated with rHuPSP94 at a concentration of 1 µg/kg/day was 65 % (p=0.010) (p values measured by unpaired Student's t-test at p<0.05 as cut-off limit).

EXAMPLE 10

IN-VIVO EXPERIMENT USING PC-3 CELL LINE

(Figure 14)

35 PC-3 human prostate tumor was obtained from ATCC (ATCC 1435). PC-3 cells were grown in RPMI media containing 10 % (v/v) of fetal calf serum and were harvested in the logarithmic phase of growth by trypsinization. Cells were centrifuged at 1200 rotation per minute (rpm) and washed three times with Hanks balanced salt solution (HBSS). Following washing, cells were counted and adjusted to a concentration of 1×10^7 cells/ml in HBSS. A 0.1 ml volume of tumor cell inoculum containing 1×10^6 cells was administered subcutaneously into the two opposite flank region of each Nude mouse (Nu/Nu, BALB/c background). Tumor growth was monitored for approximately 18 days. Once tumor growth has been established (volume of tumor reached a volume of 50 mm³) treatment

with rHuPSP94 (SEQ ID NO: 2) was initiated and was performed once a day for 14 days by the subcutaneous route. Based on the assigned treatment groups illustrated in table 4.

5 TABLE 4

Treatment group	Test control articles	Dose Level (µg/kg/day)	Dose concentration (µg/mg)	No. of animal
1 Negative control	PBS	0	0	8
2 Positive control	Doxorubicin	5000	2500	8
3	rHuPSP94	1	0.5	8
4	rHuPSP94	10	5	8
5	rHuPSP94	100	50	8
6	rHuPSP94	1000	500	8

10 Results of this experiment (Figure 14) demonstrated tumor growth reduction in the group of mice treated with rHuPSP94 at a dosage level of 1 µg/kg body weight per day. This reduction was similar to that observed for Doxorubicin (given at 5 mg/kg/day) which is a chemotherapeutic agent used as reference gold standard.

15

EXAMPLE 11

IN-VIVO EXPERIMENT USING PC-3 CELL LINE

(Figures 15-17)

20

PC-3 human prostate tumor (ATCC 1435) obtained from ATCC was implanted bilaterally into nude mice and tumor growth was monitored for approximately 18 days. PC-3 cells were injected once subcutaneously into each flank of the mice. Once tumor growth has been established (i.e., volume of tumor reached 0.25 to 0.50 cm³) the treatment with decapeptide (SEQ ID NO: 3), native PSP94 (SEQ ID NO: 1) and control scrambled polypeptide PB111 was initiated and was performed once a day for 14 days by the subcutaneous route based on the treatment groups (randomly assigned) illustrated in table 5.

30

TABLE 5

Treatment groups	Test and control articles	Dose Level ($\mu\text{g/kg/day}$)	Dose concentration ($\mu\text{g/mg}$)	No. of animal
1(Negative control)	PBS	0	0	4
3	Decapeptide (SEQ ID NO: 3)	1	0.5	4
4	Decapeptide (SEQ ID NO: 3)	10	5	4
5	Decapeptide (SEQ ID NO: 3)	100	50	4
6	Decapeptide (SEQ ID NO: 3)	1000	500	4
7	Native PSP94 (SEQ ID NO: 1)	1	0.5	4
8	Native PSP94 (SEQ ID NO: 1)	10	5	4
10	Native PSP94 (SEQ ID NO: 1)	100	50	4
11	Native PSP94 (SEQ ID NO: 1)	1000	500	4
12	Scrambled polypeptide(PB111)	1	0.5	4
13	Scrambled polypeptide(PB111)	10	5	4
14	Scrambled polypeptide(PB111)	100	50	4
15	Scrambled polypeptide(PB111)	1000	500	4

Figure 15 represents results obtained for tumor-implanted nude mice treated with the decapeptide (SEQ ID NO: 3) compared to a non-treated control. Figure 16 represents results obtained for tumor-implanted nude mice treated with scrambled polypeptide PB111 compared to a non-treated control. Figure 17 represents results obtained for tumor-implanted nude mice treated with native PSP94 (SEQ ID NO: 1) compared to a non-treated control. Results of these experiments (Figures 15-17) indicate a significant ($p < 0.05$) tumor growth reduction in mice treated with the decapeptide (SEQ ID NO: 3) at a dosage level of 10 $\mu\text{g/kg}$ body weight per day.

EXAMPLE 12
MANUFACTURING AND PREPARATION OF POLYPEPTIDES

5 PSP94 derived polypeptides including PCK3145 (SEQ ID NO: 5)
were synthesized using the Fmoc and BOC solid phase polypeptide
synthesis method (Merrifield, B., Science, 232: 341-347, 1986).
Polypeptides were analyzed in order to determine their identity by
Mass Spectral Analysis. Polypeptide samples were analyzed using the
10 PerSeptive Biosystems (Framingham, MA), with Voyager-DE MALDI-TOF
mass spectrometer using 337 nm light from a nitrogen laser. About 50
scans were averaged for each analysis. A sample from the native PSP94
was also analyzed under similar conditions for comparison.
Polypeptides were weighed on a Mettler AE 163 micro-balance. The
15 measurements were to nearest 0.1 mg. The polypeptides were
reconstituted in 10 mM PBS pH 7.3 to a final concentration of 1 and 5
mg/ml. The polypeptides dissolved relatively well and were filter
sterilized through a 0.2 μ m syringe filter. Aliquots of 2 ml/tube
were made and stored at -80 °C.

20 The pH of the polypeptides was measured after reconstitution to
ensure that possible differences in pH would not be a factor of
variation. The pH values of each solution were taken at three
concentrations: neat, 100 μ g/ml and 12.5 μ g/ml. The pH range was
25 approximately from 7.0 to 7.5. This did not make a significant
difference in the outcome of the test as cells survive very well
within this pH range. To change the concentrations to molar values,
the approximate volume of the 1 mg/ml stocks were diluted in PBS pH
7.3. All stocks were made to contain 450 μ M polypeptide solutions.
30 When fresh stocks of polypeptide were to be reconstituted, it was
done directly to 450 μ M concentration in PBS pH 7.3.

After our initial screening and confirmation of the inhibitory
activity of the polypeptide on the growth of the PC-3 cells, a GMP
35 manufactured polypeptide was tested. This polypeptide was weighed and
dissolved in PBS and 2 mg/ml stock solution was prepared, sterile
filtered through a 0.2 μ m syringe filter and stored at in -80 °C.

EXAMPLE 13

EFFECT OF PCK3145 ON IN-VITRO PC-3 CELLS (MTS ASSAY (Figures 18-21))

PCK3145, manufactured as set forth in example 12, was evaluated as a lead candidate product in tumor growth inhibition.

The biological activity of PCK3145 was determined by its growth inhibitory effect on the human prostate cancer cell line PC-3 using the MTS/PMS kit (Promega). This assay measures the mitochondrial activity of the live cells. The basic principle of this method involves the fact that the mitochondrial enzymes of the live cells metabolize the MTS/PMS dyes forming a brown colored precipitate which can be measured as optical density (OD) by absorption at 490 nm in a spectrophotometer. Therefore, the OD values are proportional to the number of living cells.

In addition, a visual observation of the cells was also done to check the cell morphology, which could also be indicative of cell growth. The following conditions for MTS assay were used: PC-3 (ATCC, Lot AT06), passage number $n \geq 70$, cell line adapted to grow in serum-free OPTI-MEM and in RPMI supplemented with BSA (50 $\mu\text{g/ml}$) and Ferrous Sulfate (0.1 μM), continuous exposure for up to 72 hours without changing media (i.e., adding PCK3145 at 2X concentration directly to wells and diluting it 1:2 to 1X to minimize cell manipulation and avoid detachment). As indicated in Figure 18, PCK3145 was assessed at the following concentrations: 12.5, 25, 50, 100, 200, 300 and 400 $\mu\text{g/ml}$ on PC-3 cells (ATCC) grown in supplemented media. The MTS tests were repeated 5 times and a dose dependent inhibitory effect on the growth of PC-3 cells was consistently reproducible demonstrating approximately 40 % cell growth inhibition at the highest PCK3145 concentration of 400 $\mu\text{g/ml}$.

With the availability of GMP (good manufacturing practice) grade polypeptide the MTS assays were repeated to check the reproducibility and cytotoxicity against PC-3 cells. In parallel PC-3 cells were also treated with the native PSP94 as a reference positive control and with no treatment (negative control, i.e., cont.). Figure 19 shows the results of the MTS assay where 4000 cells were seeded and exposed to PCK3145 (GMP grade) for 48 hours. A 30 % growth inhibitory effect was observed following treatment with

PCK3145 at 500 µg/ml. This effect was increased to approximately 40 % after 72 hours of exposure (Figure 20). In a repeat experiment a 48 hours exposure to the polypeptide at 500 µg/ml resulted in only 20-22 % growth inhibition, however this effect increased to 30 % after 72 hours exposure (Figure 21). Despite assay to assay variability reflected by the state of cell growth in vitro, polypeptide PCK3145 exhibited a significant cell growth inhibition.

EXAMPLE 14

EFFECT OF PCK3145 ON IN-VITRO PC-3 CELLS [³H]-THYMIDINE UPTAKE ASSAY (Figures 22-24)

[³H]-Thymidine uptake assay involves [³H]-Thymidine incorporation into cellular DNA of actively proliferating cells. [³H]-Thymidine uptake assay measures the proliferative index of the cells versus the MTS assay, which quantifies the number of lived cells following treatment. The anti-proliferative effects of PCK3145 and two other synthetic polypeptides derived from the amino and carboxy terminus ends of PSP94 (SEQ ID NO: 4 and NO: 6, respectively) as well as the decapeptide (SEQ ID NO: 3) previously shown to mimic the biological action of native PSP94 were assessed in [³H]-Thymidine uptake assay on PC-3 cells. Two separate experiments were conducted with GMP-grade PCK3145.

As shown in the Figures 22 and 23, polypeptide PCK3145 exhibited a significant proliferation inhibition activity reflected in the percentage of [³H]-Thymidine uptake. In the first experiment, a reduction of nearly 40 % in [³H]-Thymidine uptake was observed at PCK3145 concentration of 200 µg/ml. In the second experiment, although a two fold higher concentration of the PCK3145 was used (i.e., 400 µg/ml) only a 25 % inhibition was observed. Despite assay to assay variation the overall degree of proliferative inhibitory effect against PC-3 cell was markedly evident with the GMP grade material. Treatment of PC-3 cells with the native PSP94 used as a positive reference standard, exhibited a significant dose dependent reduction in cell proliferation with almost 50 % reduction in the [³H]-Thymidine uptake following 72 hours exposure (Figure 24).

EXAMPLE 15
IN VITRO EFFECT OF PCK3145 ON PC-3 CELLS
(APOPTOSIS-Figure 25)

Apoptosis of PC-3 cells, following a 72 hours exposure to PCK3145 at 500 µg/ml concentration, was evaluated in supplemented media by DNA fragmentation assay. Doxorubicin was used as a reference positive control. Untreated cells and PCK3145-treated cells were harvested and the DNA was isolated. Isolated DNA was run on a 1.2 % agarose gel containing Ethidium Bromide (EtBr). As shown in Figure 25 treatment of PC-3 cells with polypeptide PKC3145 resulted in DNA fragmentation evidenced by the ladder formation seen for fragmented DNA. Lane 1 of the gel illustrated in figure 25 represents the DNA marker (100 base pair DNA ladder). Lane 2 of the gel illustrated in figure 25 represents a control of untreated PC-3 cells. Lane 3 of the gel illustrated in figure 25 represents DNA laddering effect observed for cells treated with doxorubicin at a concentration of 2 µg/ml. Lane 4 of the gel illustrated in figure 25 represents DNA laddering effect observed for cells treated with PCK3145 (SEQ ID NO: 5).

EXAMPLE 16
IN VIVO EXPERIMENTS USING HUMAN PC-3 PROSTATE CANCER CELL LINE
(Figures 26-27)

Studies PC3-6 and PC3-12 (Figures 26 - 27) are consecutive group experiments designed to characterize the in vivo activity of PCK3145 in the human PC-3 prostate cancer nude mouse xenograft model and to explore relationships between dose, route and schedule of administration and the efficacy parameters of tumor growth (volume).

PC-3 cells harvested in mid-log phase were inoculated at 5×10^6 cells per mice via the subcutaneous route in the mice's back area. Tumors grown from this inoculum were excised at approximately day 32 to 35 post-tumor implantation (p.t.i) when tumor volume reached 200-300 mm³ (i.e., cu mm). The necrotic tissue was removed and the viable tumor mass cut into small pieces (approximately 1 to 3 mm³) were implanted SC in the flank region at two opposite sites of the mouse. Treatment with various concentrations of PCK3145 was initiated at day 3 post-tumor implantation (p.t.i) and was continued daily for 21 days. Subcutaneous injections were done below tumor growth sites. Intra-peritoneal injections were performed in the

abdominal region. Intra-venous injections were performed via the lateral tail vein. The experiment was terminated 24 hours after the last treatment. Tumor measurements were taken at Days 11, 14, 16, 18, 20, 22 and 24 post-tumor implantation (p.t.i). Tumor volumes were calculated according to formula ($axb^2 \times 0.5$), where a - is the length of the long diameter, and b-is the width of the perpendicular small diameter.

Study No: PC3-6 illustrates the efficacy of PCK3145, injected subcutaneously, in tumor growth retardation in Nude mice, which have received PC-3 implants. Mice were separated in different group each receiving various amounts of PCK3145 (SEQ ID NO: 5) or control reagents. The different groups used in these experiments are illustrated in table 6 below. Each group contained 10 mice.

Doxorubicin was administered as single bolus intra-venous injection on days 3 and 11 post-tumor implantation (p.t.i).

TABLE 6

Treatment group	Test and control articles	Dose Level ($\mu\text{g/kg/day}$)	No. of animals	No. of tumors
1 Negative control	PBS	0	10	20
2 Positive control	Doxorubicin	10000	10	20
3	PCK3145	0.1	10	20
4	PCK3145	1	10	20
5	PCK3145	10	10	20

Results of this study (Figure 26) demonstrated a significant PC-3 tumor growth retardation following treatment with PCK3145 at 10 $\mu\text{g/kg/day}$. This anti-tumor effect was evidenced by a statistically significant decrease in percentage of tumor growth observed at days 11, 14, 16, 18, 21 and 24 after tumor implantation with respective p-values ranging from $p=0.001$ to 0.002 , in comparison to the control PBS-treated group (p values measured by unpaired Student's t-test at $p<0.05$ as cut-off limit). Doxorubicin, a potent chemotherapeutic agent, was used as reference gold standard and demonstrated a highly significant anti-tumor therapeutic effect. ANOVA analysis of variance, Dunnett's test, Kruskal-Wallis and Dunn's test analysis of data confirmed statistical significance of the observed anti-tumor effect.

Study No: PC3-12 illustrates the efficacy of PCK3145 in tumor growth retardation in Nude mice, which have received PC-3 implants. Mice were separated in different group each receiving various amounts of PCK3145 (SEQ ID NO: 5) or control reagents. PCK3145 was injected either through intra-venous or intra-peritoneal route. The different groups used in these experiments are illustrated in table 7 below. Each group contained 9 mice.

TABLE 7

Treatment groups	Test and control articles	Dose level (µg/kg/day)	No. of animals	No. of tumors
1 Negative control	PBS	0	9	18
2	PCK3145 IV	10	9	18
3	PCK3145 IV	100	9	18
4	PCK3145 IV	500	9	18
5	PCK3145 IV	1000	9	18
6	PCK3145 IP	100	9	18
7	PCK3145 IP	1000	9	18

Results of this experiment (Figure 27) demonstrated a significant tumor growth retardation following treatment with PCK3145 at 100 µg/kg/day via the intra-venous route. This effect was statistically significant at days 13, 17 and 20 after tumor implantation when compared by Student's t-test (p-values were p=0.005, 0.025 and 0.011, respectively for each time-point) (p values measured by unpaired Student's t-test at p<0.05 as cut-off limit). No significant anti-tumor effect was observed following PCK3145 treatment at the other dosage levels of 10, 500 and 1000 µg/kg/day injected via the intra-venous route. However a trend towards significance was observed following treatment with 500 and 1000 µg/kg/day doses of PCK3145. Treatment of mice with PCK3145 at 100 and 1000 µg/kg/day administered via the intra-peritoneal route showed a similar tumor growth retardation trend with statistically less significant difference observed at day 13 p.t.i (p=0.056) (p values measured by unpaired Student's t-test at p<0.05 as cut-off limit) at the highest dose of 1000 µg/kg/day (Figure 27).

During the course of experimentation using the human PC-3 prostate cancer nude mouse xenograft model, results obtained have

suggested that subcutaneous PCK3145 injection of mice at a site (i.e., scruff of the neck) distant from tumor site, might not be efficacious enough and will unlikely may unlikely result in an anti-tumor effect, at least in the experimental conditions tested (doses of PCK3145 tested: 10 µg/kg/day and 100 µg/kg/day). The use of the scruff of the neck as a subcutaneous injection site represents an optimal site for immune response induction rather than a route for therapeutic product administration and as such, selection of this site is expected to be a sub-optimal site for tumor efficacy evaluation.

EXAMPLE 17

IN VIVO EXPERIMENTS USING DUNNING RAT MAT LY LU PROSTATE CANCER

LINE

(Figures 28-30)

Anti-tumor efficacy evaluation of PCK3145 against Mat Ly Lu (MLL) tumor implanted in Copenhagen rats was performed. (Protocol based on S. Garde et al.; The Prostate, 22: 225-233, 1993). Mat LyLu tumor cells were harvested in mid-log phase from the culture flasks by trypsinization, were centrifuged at 1200 rotation per minute (rpm) and washed three times with Hanks balanced salt solution (HBSS). Following washing, cells were counted and adjusted to a concentration of 5×10^6 cells/ml in HBSS. A 0.1 ml volume of tumor cell inoculum containing 5×10^5 cells was administered subcutaneously into the flank region of each rat. Treatment started at day 3 post-tumor implantation (p.t.i) by local subcutaneous injection (i.e., in the shaved back area just below tumor implantation site) of various PCK3145 concentrations. This treatment was continued daily for 16 days. Experiments were terminated 24 hours after the last treatment. Tumor measurements were taken at days 7, 9, 11, 14, 16 and 18. Tumor volumes are calculated according to formula ($axb^2 \times 0.5$), where a - is the length of the long diameter, b-width of the perpendicular small diameter. At day 19 tumors of individual rats were excised and weighed.

Study No: MLL-5 illustrates the efficacy of PCK3145 (SEQ ID NO: 5) compared with polypeptide 7-21 (SEQ ID NO: 4) and polypeptide 76-94 (SEQ ID NO: 6) in tumor growth retardation in Copenhagen rats, which have received Mat Ly Lu implants. Mice were separated in different groups, each receiving various amount of PCK3145 (SEQ ID NO: 5) or control reagents. PCK3145 was injected through the

subcutaneous route. The different groups used in these experiments are illustrated in table 8 below. Each group contained 8 mice.

5 TABLE 8

Treatment groups	Test and control articles	Dose Level (µg/kg/day)	No. of animals	No. of tumors
1 Negative control	PBS	0	8	8
2	Polypeptide 7-21	10	8	8
3	Polypeptide 7-21	1	8	8
4	PCK3145	10	8	8
5	PCK3145	1	8	8
6	Polypeptide 76-94	10	8	8
7	Polypeptide 76-94	1	8	8

10 Results of this study (Figure 28) demonstrated a significant anti-tumor effect following administration of PCK3145 at 10 µg/kg/day. This was evidenced by a significant tumor volume reduction at days 11 (p=0.006), 13 (p=0.00001), 16 (p=0.002) and 18(p=0.004), post-tumor cell implantation compared to control PBS-
15 treated group (p values measured by unpaired Student's t-test at p<0.05 as cut-off limit). No significant effect was detectable following PCK3145 treatment at 1 µg/kg/day. It was of interest to note that the amino-terminus polypeptide 7-21 also demonstrated comparable anti-tumor effect, which was also observed in the PC-3
20 nude mouse xenograft model, indicating the possibility of an overlapping active site between the N-terminus and the central regions of the PSP94 protein. This was evidenced by a significant tumor volume reduction observed at day 13 (p=0.05), 16 (p=0.00005), and 18 (p=0.01) in mice treated with polypeptide 7-21) (p values
25 measured by unpaired Student's t-test at p<0.05 as cut-off limit).

Study No: MLL-6 illustrates the efficacy of PCK3145 (SEQ ID NO: 5) in tumor growth retardation in Copenhagen rats, which have received Mat Ly Lu implants. Mice were separated in different group
30 each receiving various amounts of PCK3145 (SEQ ID NO: 5) or control reagents. PCK3145 was injected through the subcutaneous route. The

different groups used in these experiments are illustrated in table 9 below. Each group contained 8 mice. Doxorubicin was administered as single bolus via intra-venous injection on day 3 p.t.i.

5

TABLE 9

Treatment groups	Test and control articles	Dose level ($\mu\text{g/kg/day}$)	No. of animals	No. of tumors
1 (Negative control)	PBS	0	8	8
2	Doxorubicin	5000	8	8
3	PCK3145	10	8	8
4	PCK3145	100	8	8
5	Scrambled polypeptide	10	8	8
6	Scrambled polypeptide	100	8	8

10

Results of this study (Figures 29 and 30) demonstrated a significant dose-dependent anti-tumor effect following administration of PCK3145 at 10 and 100 $\mu\text{g/kg/day}$. This was evidenced by a significant tumor volume reduction (31 % over control) following PCK3145 treatment especially with 100 $\mu\text{g/kg/day}$ at days 14, 16 and 18 post-tumor cell implantation (Figure 29). The p-value versus negative control-treated group (i.e., scrambled polypeptide (PB111)) was highly significant at $p=0.0000062$ (p values measured by unpaired Student's t-test at $p<0.05$ as cut-off limit). A moderate extent of growth retardation (marginal statistical significance at $p=0.03$ versus control PBS-treated group) was also observed following treatment with scrambled polypeptide at a concentration of 100 $\mu\text{g/kg/day}$ (Figure 29) (p values measured by unpaired Student's t-test at $p<0.05$ as cut-off limit). Doxorubicin treatment was highly significant resulting in over 80 % reduction in tumor volumes. This anti-tumor effect of PCK3145 at 100 $\mu\text{g/kg/day}$ was also reproduced following analysis of the tumor weights data. As shown in figure 30, (tumor weight data) a significant reduction in tumor weights ($p=0.0003$) was observed on day 18 p.t.i (p values measured by unpaired Student's t-test at $p<0.05$ as cut-off limit). This represented a 34 % reduction in tumor mass, a 20 gram difference between the control (56.6 g) and PCK3145-treated at 100 $\mu\text{g/kg/day}$ group (37.2 g). This difference in tumor weights was also

30

statistically significant when it was compared to the tumor weights of the control scrambled polypeptide-treated rats given the same dose of 100 µg/kg/day (p=0.003) (p values measured by unpaired Student's t-test at p<0.05 as cut-off limit). Comparison of the scrambled polypeptide treated tumor weights with that of control PBS-untreated tumor weights was not statistically significant (p=0.06) (p values measured by unpaired Student's t-test at p<0.05 as cut-off limit).

EXAMPLE 18

EFFICACY OF PCK3145 AND TAXOTERE COMBINATION TREATMENT

In order to test for the efficacy of combination treatment, in tumor growth retardation, PCK3145 and taxotere (i.e., docetaxel) were co-administered in Nude mice previously inoculated with PC-3 tumor cells. Mice were separated in different groups each receiving PCK3145 alone or PCK3145 in combination with taxotere (administered by separate routes) or control reagent (i.e., PBS). In this experiment, the combination treatment was initiated against relatively large tumor burdens. Tumors were allowed to grow beyond the 50 to 60 mm³ size at which PCK3145 treatment usually becomes inefficient. PCK3145 was injected through intravenous route every other day for 28 days starting from day 1 when 50 to 60 mm³ size subcutaneous tumors were apparent. Taxotere was injected by intra-peritoneal route at a sub-optimal concentration of 2 mg/kg on days 4 and 11 after subcutaneous tumors were evident. The different groups used in this experiment are illustrated in table 10 below. Each group contained 11 mice.

TABLE 10

Treatment groups	Test and control articles	Dose level (µg/kg)	No. of animals	No of tumors
1. Negative control	PBS	0	11	11
2. Positive control	Taxotere	2000	11	11
3.	PCK3145	100	11	11
4.	PCK3145 + taxotere	100 + 2000	11	11

Results of this experiment (Figure 31) demonstrate a significant tumor growth retardation following combination treatment of PCK3145 and taxotere. This effect is statistically significant at days 19 and 22 post-tumor cell inoculation when compared by Student's
5 t-test ($p=0.02$ at day 19 and $p=0.047$ at day 22), (p-values are measured by unpaired Student's t-test at $p<0.05$ as a cut-off limit) and was markedly better than taxotere administered alone at the same dose of 2 mg/kg (suboptimal dose).

10 All publications and patent applications cited in this specification are herein incorporated by reference as if each individual publication or patent application were specifically and individually indicated to be incorporated by reference. The citation
15 of any publication is for its disclosure prior to the filing date and should not be construed as an admission that the present invention is not entitled to antedate such publication by virtue of prior invention.

20 Although the foregoing invention has been described in some detail by way of illustration and example for purposes of clarity of understanding, it is readily apparent to those of ordinary skill in the art in light of the teachings of this invention that certain changes and modifications may be made thereto without departing from the spirit or scope of the appended claims.
25

SEQUENCE LISTING

5 (1) GENERAL INFORMATION:

(i) APPLICANT: PROCYON BIOPHARMA INC.

10 (ii) TITLE OF INVENTION: PHARMACEUTICAL PREPARATIONS AND
METHODS FOR INHIBITING TUMORS

(iii) NUMBER OF SEQUENCES: 92

(iv) CORRESPONDENCE ADDRESS:

15 (A) ADRESSEE: BROULLETTE KOSIE
(B) STREET: 1100 RENE-LESVEQUE BLVD WEST
(C) PROV/STATE: QUEBEC
(D) COUNTRY: CANADA
20 (E) POSTAL/ZIP CODE: H3B 5C9

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: FLOPPY DISK
(B) COMPUTER: IBM PC COMPATIBLE
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
25 (D) SOFTWARE: ASCII (TEXT)

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER:
(B) FILING DATE:
30 (C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: 2,321,256
(B) FILING DATE: 2000-10-16
35 (C) CLASSIFICATION: A61K-38/17

(A) APPLICATION NUMBER: 2,355,334
(B) FILING DATE: 2001-08-20

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45 (E) FAX NO.: (514) 397 8515

(2) INFORMATION FOR SEQ ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:

50 (A) LENGTH: 94 AMINO ACIDS
(B) TYPE: AMINO ACIDS
(C) STRANDEDNESS: SINGLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

55 (iii) HYPOTHETICAL:

(iv) ANTI-SENSE:

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(A) ORGANISM:

60 (vii) IMMEDIATE SOURCE:

(viii) POSITION IN GENOME

(A) CHROMOSOME/SEGMENT:

(B) MAP POSITION:

(C) UNITS:

65 (ix) FEATURE:

(A) NAME/KEY:
 (B) LOCATION:
 (C) IDENTIFICATION METHOD:
 (D) OTHER INFORMATION:
 5 (x) PUBLICATION INFORMATION:
 (A) AUTHORS:
 (B) TITLE:
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 10 (D) VOLUME:
 (E) ISSUE:
 (F) PAGES:
 (G) DATE:
 (H) DOCUMENT NO.:
 15 (I) FILING DATE:
 (J) PUBLICATION DATE:
 (K) RELEVANT RESIDUES IN SEQ ID NO:1:

 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
 20 Ser Cys Tyr Phe Ile Pro Asn Glu Gly Val Pro Gly Asp Ser Thr Arg
 1 5 10 15
 Lys Cys Met Asp Leu Lys Gly Asn Lys His Pro Ile Asn Ser Glu Trp
 20 25 30
 25 Gln Thr Asp Asn Cys Glu Thr Cys Thr Cys Tyr Glu Thr Glu Ile Ser
 35 40 45
 30 Cys Cys Thr Leu Val Ser Thr Pro Val Gly Tyr Asp Lys Asp Asn Cys
 50 55 60
 Gln Arg Ile Phe Lys Lys Glu Asp Cys Lys Tyr Ile Val Val Glu Lys
 65 70 75 80
 35 Lys Asp Pro Lys Lys Thr Cys Ser Val Ser Glu Trp Ile Ile
 85 90

 40 (2) INFORMATION FOR SEQ ID NO: 2:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 102 AMINO ACIDS
 (B) TYPE: AMINO ACIDS
 (C) STRANDEDNESS: SINGLE
 45 (D) TOPOLOGY: LINEAR
 (ii) MOLECULE TYPE: PROTEIN

 (vi) ORIGINAL SOURCE:
 50 (A) ORGANISM:

 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

 55 Glu Ala Glu Ala Tyr Val Glu Phe Ser Cys Tyr Phe Ile Pro Asn Glu
 1 5 10 15
 Gly Val Pro Gly Asp Ser Thr Arg Lys Cys Met Asp Leu Lys Gly Asn
 20 25 30
 60 Lys His Pro Ile Asn Ser Glu Trp Gln Thr Asp Asn Cys Glu Thr Cys
 35 40 45
 65 Thr Cys Tyr Glu Thr Glu Ile Ser Cys Cys Thr Leu Val Ser Thr Pro
 50 55 60

Val Gly Tyr Asp Lys Asp Asn Cys Gln Arg Ile Phe Lys Lys Glu Asp
65 70 75 80
5 Cys Lys Tyr Ile Val Val Glu Lys Lys Asp Pro Lys Lys Thr Cys Ser
85 90 95
Val Ser Glu Trp Ile Ile
100

10

(2) INFORMATION FOR SEQ ID NO: 3:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 AMINO ACIDS
(B) TYPE: AMINO ACIDS
(C) STRANDEDNESS: SINGLE
(D) TOPOLOGY: LINEAR
(ii) MOLECULE TYPE: PROTEIN

15

(vi) ORIGINAL SOURCE:
(A) ORGANISM:

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

25 Tyr Thr Cys Ser Val Ser Glu Pro Gly Ile
1 5 10

30

(2) INFORMATION FOR SEQ ID NO: 4:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 AMINO ACIDS
(B) TYPE: AMINO ACIDS
(C) STRANDEDNESS: SINGLE
(D) TOPOLOGY: LINEAR
(ii) MOLECULE TYPE: PROTEIN

35

(vi) ORIGINAL SOURCE:
(A) ORGANISM:

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

45 Asn Glu Gly Val Pro Gly Asp Ser Thr Arg Lys Cys Met Asp Leu
1 5 10 15

50

(2) INFORMATION FOR SEQ ID NO: 5:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 AMINO ACIDS
(B) TYPE: AMINO ACIDS
(C) STRANDEDNESS: SINGLE
(D) TOPOLOGY: LINEAR
(ii) MOLECULE TYPE: PROTEIN

55

(vi) ORIGINAL SOURCE:
(A) ORGANISM:

60

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

65 Glu Trp Gln Thr Asp Asn Cys Glu Thr Cys Thr Cys Tyr Glu Thr
1 5 10 15

5 (2) INFORMATION FOR SEQ ID NO: 6:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 19 AMINO ACIDS
 (B) TYPE: AMINO ACIDS
 (C) STRANDEDNESS: SINGLE
 (D) TOPOLOGY: LINEAR
 10 (ii) MOLECULE TYPE: PROTEIN
 (vi) ORIGINAL SOURCE:
 (A) ORGANISM:
 15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:
 Ile Val Val Glu Lys Lys Asp Pro Lys Lys Thr Cys Ser Val Ser Glu
 1 5 10 15
 20 Trp Ile Ile

(2) INFORMATION FOR SEQ ID NO: 7:
 25 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 26
 (B) TYPE: NUCLEOTIDES
 (C) STRANDEDNESS: SINGLE
 (D) TOPOLOGY: LINEAR
 30 (ii) MOLECULE TYPE: DNA
 (vi) ORIGINAL SOURCE:
 (A) ORGANISM:
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:
 35 GGGAAGAATT CTCATGCTAT TTCATA 26

(2) INFORMATION FOR SEQ ID NO: 8:
 40 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 21
 (B) TYPE: NUCLEOTIDES
 (C) STRANDEDNESS: SINGLE
 (D) TOPOLOGY: LINEAR
 45 (ii) MOLECULE TYPE: DNA
 (vi) ORIGINAL SOURCE:
 (A) ORGANISM:
 50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:
 TGGATATCTG CAGAATTCGG C 21

55 2) INFORMATION FOR SEQ ID NO: 9:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH:
 (B) TYPE: NUCLEOTIDES
 (C) STRANDEDNESS: SINGLE
 60 (D) TOPOLOGY: LINEAR
 (ii) MOLECULE TYPE:

(vi)ORIGINAL SOURCE:

(A) ORGANISM:

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

TCATGCTATT TCATACCTAA TGAGGGAGTT CCAGGAGATT CAACCAGGAA ATGCATGGAT 60
CTCAAAGGAA ACAAACACCC AATAAACTCG GAGTGGCAGA CTGACAACTG TGAGACATGC 120
10 ACTTGCTACG AAACAGAAAT TTCATGTTGC ACCCTTGTTT CTACACCTGT GGGTTATGAC 180
AAAGACAACT GCCAAAGAAT CTTCAAGAAG GAGGACTGCA AGTATATCGT GGTGGAGAAG 240
15 AAGGACCCAA AAAAGACCTG TTCTGTCAGT GAATGGATAA TCTAA 285

2) INFORMATION FOR SEQ ID NO: 10:

20 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 16

(B) TYPE: AMINO ACID

(C) STRANDEDNESS: SINGLE

(D) TOPOLOGY: LINEAR

25 (ii)MOLECULE TYPE:

(vi)ORIGINAL SOURCE:

(A) ORGANISM:

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

Glu Trp Gln Thr Asp Asn Cys Glu Thr Cys Thr Cys Tyr Glu Thr Glu
1 5 10 15

35

2) INFORMATION FOR SEQ ID NO: 11:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 17

(B) TYPE: AMINO ACID

40 (C) STRANDEDNESS: SINGLE

(D) TOPOLOGY: LINEAR

(ii)MOLECULE TYPE:

(vi)ORIGINAL SOURCE:

45 (A) ORGANISM:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

50 Glu Trp Gln Thr Asp Asn Cys Glu Thr Cys Thr Cys Tyr Glu Thr Glu
1 5 10 15

Ile

2) INFORMATION FOR SEQ ID NO: 12:

55 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 18

(B) TYPE: AMINO ACID

(C) STRANDEDNESS: SINGLE

(D) TOPOLOGY: LINEAR

60 (ii)MOLECULE TYPE:

(vi)ORIGINAL SOURCE:

(A) ORGANISM:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

5 Glu Trp Gln Thr Asp Asn Cys Glu Thr Cys Thr Cys Tyr Glu Thr Glu
1 5 10 15
Ile Ser

10 2) INFORMATION FOR SEQ ID NO: 13:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 19

(B) TYPE: AMINO ACID

(C) STRANDEDNESS: SINGLE

15 (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE:

(vi) ORIGINAL SOURCE:

(A) ORGANISM:

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:

25 Glu Trp Gln Thr Asp Asn Cys Glu Thr Cys Thr Cys Tyr Glu Thr Glu
1 5 10 15
Ile Ser Cys

30 2) INFORMATION FOR SEQ ID NO: 14:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20

(B) TYPE: AMINO ACID

(C) STRANDEDNESS: SINGLE

35 (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE:

(vi) ORIGINAL SOURCE:

(A) ORGANISM:

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:

45 Glu Trp Gln Thr Asp Asn Cys Glu Thr Cys Thr Cys Tyr Glu Thr Glu
1 5 10 15
Ile Ser Cys Cys
20

50

2) INFORMATION FOR SEQ ID NO: 15:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 21

(B) TYPE: AMINO ACID

55 (C) STRANDEDNESS: SINGLE

(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE:

(vi) ORIGINAL SOURCE:

60

(A) ORGANISM:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15:

Glu Trp Gln Thr Asp Asn Cys Glu Thr Cys Thr Cys Tyr Glu Thr Glu
 1 5 10 15

5 Ile Ser Cys Cys Thr
 20

2) INFORMATION FOR SEQ ID NO: 16:

10 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 22
 (B) TYPE: AMINO ACID
 (C) STRANDEDNESS: SINGLE
 (D) TOPOLOGY: LINEAR

15 (ii) MOLECULE TYPE:

(vi) ORIGINAL SOURCE:

(A) ORGANISM:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 16:

20 Glu Trp Gln Thr Asp Asn Cys Glu Thr Cys Thr Cys Tyr Glu Thr Glu
 1 5 10 15

25 Ile Ser Cys Cys Thr Leu
 20

2) INFORMATION FOR SEQ ID NO: 17:

30 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 23
 (B) TYPE: AMINO ACID
 (C) STRANDEDNESS: SINGLE
 (D) TOPOLOGY: LINEAR

35 (ii) MOLECULE TYPE:

(vi) ORIGINAL SOURCE:

(A) ORGANISM:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 17:

40 Glu Trp Gln Thr Asp Asn Cys Glu Thr Cys Thr Cys Tyr Glu Thr Glu
 1 5 10 15

45 Ile Ser Cys Cys Thr Leu Val
 20

2) INFORMATION FOR SEQ ID NO: 18:

50 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 24
 (B) TYPE: AMINO ACID
 (C) STRANDEDNESS: SINGLE
 (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE:

55 (vi) ORIGINAL SOURCE:

(A) ORGANISM:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 18:

60 Glu Trp Gln Thr Asp Asn Cys Glu Thr Cys Thr Cys Tyr Glu Thr Glu
 1 5 10 15

65 Ile Ser Cys Cys Thr Leu Val Ser
 20

2) INFORMATION FOR SEQ ID NO: 19:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 25

(B) TYPE: AMINO ACID

(C) STRANDEDNESS: SINGLE

(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE:

(vi) ORIGINAL SOURCE:

(A) ORGANISM:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 19:

Glu Trp Gln Thr Asp Asn Cys Glu Thr Cys Thr Cys Tyr Glu Thr Glu
 1 5 10 15

Ile Ser Cys Cys Thr Leu Val Ser Thr
 20 25

2) INFORMATION FOR SEQ ID NO: 20:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 26

(B) TYPE: AMINO ACID

(C) STRANDEDNESS: SINGLE

(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE:

(vi) ORIGINAL SOURCE:

(A) ORGANISM:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 20:

Glu Trp Gln Thr Asp Asn Cys Glu Thr Cys Thr Cys Tyr Glu Thr Glu
 1 5 10 15

Ile Ser Cys Cys Thr Leu Val Ser Thr Pro
 20 25

2) INFORMATION FOR SEQ ID NO: 21:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 27

(B) TYPE: AMINO ACID

(C) STRANDEDNESS: SINGLE

(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE:

(vi) ORIGINAL SOURCE:

(A) ORGANISM:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 21:

Glu Trp Gln Thr Asp Asn Cys Glu Thr Cys Thr Cys Tyr Glu Thr Glu
 1 5 10 15

Ile Ser Cys Cys Thr Leu Val Ser Thr Pro Val
 20 25

2) INFORMATION FOR SEQ ID NO: 22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28
(B) TYPE: AMINO ACID
(C) STRANDEDNESS: SINGLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE:

(vi) ORIGINAL SOURCE:

(A) ORGANISM:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 22:

15 Glu Trp Gln Thr Asp Asn Cys Glu Thr Cys Thr Cys Tyr Glu Thr Glu
1 5 10 15
Ile Ser Cys Cys Thr Leu Val Ser Thr Pro Val Gly
20 25

2) INFORMATION FOR SEQ ID NO: 23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29
(B) TYPE: AMINO ACID
(C) STRANDEDNESS: SINGLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE:

(vi) ORIGINAL SOURCE:

(A) ORGANISM:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 23:

35 Glu Trp Gln Thr Asp Asn Cys Glu Thr Cys Thr Cys Tyr Glu Thr Glu
1 5 10 15
Ile Ser Cys Cys Thr Leu Val Ser Thr Pro Val Gly Tyr
20 25

2) INFORMATION FOR SEQ ID NO: 24:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30
(B) TYPE: AMINO ACID
(C) STRANDEDNESS: SINGLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE:

(vi) ORIGINAL SOURCE:

(A) ORGANISM:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 24:

55 Glu Trp Gln Thr Asp Asn Cys Glu Thr Cys Thr Cys Tyr Glu Thr Glu
1 5 10 15
Ile Ser Cys Cys Thr Leu Val Ser Thr Pro Val Gly Tyr Asp
20 25 30

2) INFORMATION FOR SEQ ID NO: 25:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 31
 (B) TYPE: AMINO ACID
 (C) STRANDEDNESS: SINGLE
 (D) TOPOLOGY: LINEAR
 5 (ii) MOLECULE TYPE:
 (vi) ORIGINAL SOURCE:
 (A) ORGANISM:
 10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 25:

 Glu Trp Gln Thr Asp Asn Cys Glu Thr Cys Thr Cys Tyr Glu Thr Glu
 1 5 10 15
 15 Ile Ser Cys Cys Thr Leu Val Ser Thr Pro Val Gly Tyr Asp Lys
 20 25 30

 20 2) INFORMATION FOR SEQ ID NO: 26:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 32
 (B) TYPE: AMINO ACID
 (C) STRANDEDNESS: SINGLE
 25 (D) TOPOLOGY: LINEAR
 (ii) MOLECULE TYPE:
 (vi) ORIGINAL SOURCE:
 (A) ORGANISM:
 30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 26:

 Glu Trp Gln Thr Asp Asn Cys Glu Thr Cys Thr Cys Tyr Glu Thr Glu
 1 5 10 15
 35 Ile Ser Cys Cys Thr Leu Val Ser Thr Pro Val Gly Tyr Asp Lys Asp
 20 25 30

 40 2) INFORMATION FOR SEQ ID NO: 27:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 33
 (B) TYPE: AMINO ACID
 (C) STRANDEDNESS: SINGLE
 45 (D) TOPOLOGY: LINEAR
 (ii) MOLECULE TYPE:
 (vi) ORIGINAL SOURCE:
 (A) ORGANISM:
 50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 27:
 Glu Trp Gln Thr Asp Asn Cys Glu Thr Cys Thr Cys Tyr Glu Thr Glu
 1 5 10 15
 55 Ile Ser Cys Cys Thr Leu Val Ser Thr Pro Val Gly Tyr Asp Lys Asp
 20 25 30

 Asn
 60 2) INFORMATION FOR SEQ ID NO: 28:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 34

(B) TYPE: AMINO ACID
(C) STRANDEDNESS: SINGLE
(D) TOPOLOGY: LINEAR

(ii)MOLECULE TYPE:

(vi)ORIGINAL SOURCE:

(A) ORGANISM:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 28:

10 Glu Trp Gln Thr Asp Asn Cys Glu Thr Cys Thr Cys Tyr Glu Thr Glu
1 5 10 15
Ile Ser Cys Cys Thr Leu Val Ser Thr Pro Val Gly Tyr Asp Lys Asp
20 25 30
15 Asn Cys

2) INFORMATION FOR SEQ ID NO: 29:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 35
(B) TYPE: AMINO ACID
(C) STRANDEDNESS: SINGLE
(D) TOPOLOGY: LINEAR

(ii)MOLECULE TYPE:

(vi)ORIGINAL SOURCE:

(A) ORGANISM:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 29:

30 Glu Trp Gln Thr Asp Asn Cys Glu Thr Cys Thr Cys Tyr Glu Thr Glu
1 5 10 15
Ile Ser Cys Cys Thr Leu Val Ser Thr Pro Val Gly Tyr Asp Lys Asp
35 20 25 30
Asn Cys Gln
35

2) INFORMATION FOR SEQ ID NO: 30:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 36
(B) TYPE: AMINO ACID
(C) STRANDEDNESS: SINGLE
(D) TOPOLOGY: LINEAR

(ii)MOLECULE TYPE:

(vi)ORIGINAL SOURCE:

(A) ORGANISM:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 30:

55 Glu Trp Gln Thr Asp Asn Cys Glu Thr Cys Thr Cys Tyr Glu Thr Glu
1 5 10 15
Ile Ser Cys Cys Thr Leu Val Ser Thr Pro Val Gly Tyr Asp Lys Asp
20 25 30
60 Asn Cys Gln Arg
35

2) INFORMATION FOR SEQ ID NO: 31:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 37
 (B) TYPE: AMINO ACID
 (C) STRANDEDNESS: SINGLE
 (D) TOPOLOGY: LINEAR
 (ii) MOLECULE TYPE:
 (vi) ORIGINAL SOURCE:
 (A) ORGANISM:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 31:
 Glu Trp Gln Thr Asp Asn Cys Glu Thr Cys Thr Cys Tyr Glu Thr Glu
 1 5 10 15
 Ile Ser Cys Cys Thr Leu Val Ser Thr Pro Val Gly Tyr Asp Lys Asp
 20 25 30
 Asn Cys Gln Arg Ile
 35

2) INFORMATION FOR SEQ ID NO: 32:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 38
 (B) TYPE: AMINO ACID
 (C) STRANDEDNESS: SINGLE
 (D) TOPOLOGY: LINEAR
 (ii) MOLECULE TYPE:
 (vi) ORIGINAL SOURCE:
 (A) ORGANISM:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 32:
 Glu Trp Gln Thr Asp Asn Cys Glu Thr Cys Thr Cys Tyr Glu Thr Glu
 1 5 10 15
 Ile Ser Cys Cys Thr Leu Val Ser Thr Pro Val Gly Tyr Asp Lys Asp
 20 25 30
 Asn Cys Gln Arg Ile Phe
 35

2) INFORMATION FOR SEQ ID NO: 33:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 39
 (B) TYPE: AMINO ACID
 (C) STRANDEDNESS: SINGLE
 (D) TOPOLOGY: LINEAR
 (ii) MOLECULE TYPE:
 (vi) ORIGINAL SOURCE:
 (A) ORGANISM:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 33:
 Glu Trp Gln Thr Asp Asn Cys Glu Thr Cys Thr Cys Tyr Glu Thr Glu
 1 5 10 15
 Ile Ser Cys Cys Thr Leu Val Ser Thr Pro Val Gly Tyr Asp Lys Asp
 20 25 30
 Asn Cys Gln Arg Ile Phe Lys
 35

2) INFORMATION FOR SEQ ID NO: 34:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 40
- (B) TYPE: AMINO ACID
- (C) STRANDEDNESS: SINGLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE:

(vi) ORIGINAL SOURCE:

- (A) ORGANISM:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 34:

Glu Trp Gln Thr Asp Asn Cys Glu Thr Cys Thr Cys Tyr Glu Thr Glu
1 5 10 15

Ile Ser Cys Cys Thr Leu Val Ser Thr Pro Val Gly Tyr Asp Lys Asp
20 25 30

Asn Cys Gln Arg Ile Phe Lys Lys
35 40

2) INFORMATION FOR SEQ ID NO: 35:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 41
- (B) TYPE: AMINO ACID
- (C) STRANDEDNESS: SINGLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE:

(vi) ORIGINAL SOURCE:

- (A) ORGANISM:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 35:

Glu Trp Gln Thr Asp Asn Cys Glu Thr Cys Thr Cys Tyr Glu Thr Glu
1 5 10 15

Ile Ser Cys Cys Thr Leu Val Ser Thr Pro Val Gly Tyr Asp Lys Asp
20 25 30

Asn Cys Gln Arg Ile Phe Lys Lys Glu
35 40

2) INFORMATION FOR SEQ ID NO: 36:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 42
- (B) TYPE: AMINO ACID
- (C) STRANDEDNESS: SINGLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE:

(vi) ORIGINAL SOURCE:

- (A) ORGANISM:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 36:

Glu Trp Gln Thr Asp Asn Cys Glu Thr Cys Thr Cys Tyr Glu Thr Glu
1 5 10 15

5 Ile Ser Cys Cys Thr Leu Val Ser Thr Pro Val Gly Tyr Asp Lys Asp
20 25 30

Asn Cys Gln Arg Ile Phe Lys Lys Glu Asp
35 40

10

2) INFORMATION FOR SEQ ID NO: 37:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 43
- (B) TYPE: AMINO ACID
- (C) STRANDEDNESS: SINGLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE:

(vi) ORIGINAL SOURCE:

(A) ORGANISM:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 37:

Glu Trp Gln Thr Asp Asn Cys Glu Thr Cys Thr Cys Tyr Glu Thr Glu
1 5 10 15

Ile Ser Cys Cys Thr Leu Val Ser Thr Pro Val Gly Tyr Asp Lys Asp
20 25 30

Asn Cys Gln Arg Ile Phe Lys Lys Glu Asp Cys
35 40

2) INFORMATION FOR SEQ ID NO: 38:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 44
- (B) TYPE: AMINO ACID
- (C) STRANDEDNESS: SINGLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE:

(vi) ORIGINAL SOURCE:

(A) ORGANISM:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 38:

Glu Trp Gln Thr Asp Asn Cys Glu Thr Cys Thr Cys Tyr Glu Thr Glu
1 5 10 15

Ile Ser Cys Cys Thr Leu Val Ser Thr Pro Val Gly Tyr Asp Lys Asp
20 25 30

Asn Cys Gln Arg Ile Phe Lys Lys Glu Asp Cys Lys
35 40

2) INFORMATION FOR SEQ ID NO: 39:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 45
- (B) TYPE: AMINO ACID
- (C) STRANDEDNESS: SINGLE
- (D) TOPOLOGY: LINEAR

(ii)MOLECULE TYPE:

(vi)ORIGINAL SOURCE:

(A) ORGANISM:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 39:

Glu Trp Gln Thr Asp Asn Cys Glu Thr Cys Thr Cys Tyr Glu Thr Glu
1 5 10 15
Ile Ser Cys Cys Thr Leu Val Ser Thr Pro Val Gly Tyr Asp Lys Asp
20 25 30
Asn Cys Gln Arg Ile Phe Lys Lys Glu Asp Cys Lys Tyr
35 40 45

2) INFORMATION FOR SEQ ID NO: 40:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 46

(B) TYPE: AMINO ACID

(C) STRANDEDNESS: SINGLE

(D) TOPOLOGY: LINEAR

(ii)MOLECULE TYPE:

(vi)ORIGINAL SOURCE:

(A) ORGANISM:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 40:

Glu Trp Gln Thr Asp Asn Cys Glu Thr Cys Thr Cys Tyr Glu Thr Glu
1 5 10 15
Ile Ser Cys Cys Thr Leu Val Ser Thr Pro Val Gly Tyr Asp Lys Asp
20 25 30
Asn Cys Gln Arg Ile Phe Lys Lys Glu Asp Cys Lys Tyr Ile
35 40 45

2) INFORMATION FOR SEQ ID NO: 41:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 47

(B) TYPE: AMINO ACID

(C) STRANDEDNESS: SINGLE

(D) TOPOLOGY: LINEAR

(ii)MOLECULE TYPE:

(vi)ORIGINAL SOURCE:

(A) ORGANISM:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 41:

Glu Trp Gln Thr Asp Asn Cys Glu Thr Cys Thr Cys Tyr Glu Thr Glu
1 5 10 15
Ile Ser Cys Cys Thr Leu Val Ser Thr Pro Val Gly Tyr Asp Lys Asp
20 25 30
Asn Cys Gln Arg Ile Phe Lys Lys Glu Asp Cys Lys Tyr Ile Val
35 40 45

2) INFORMATION FOR SEQ ID NO: 42:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 48
 (B) TYPE: AMINO ACID
 (C) STRANDEDNESS: SINGLE
 (D) TOPOLOGY: LINEAR
 (ii) MOLECULE TYPE:

(vi) ORIGINAL SOURCE:
 (A) ORGANISM:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 42:

Glu Trp Gln Thr Asp Asn Cys Glu Thr Cys Thr Cys Tyr Glu Thr Glu
 1 5 10 15
 Ile Ser Cys Cys Thr Leu Val Ser Thr Pro Val Gly Tyr Asp Lys Asp
 20 25 30
 Asn Cys Gln Arg Ile Phe Lys Lys Glu Asp Cys Lys Tyr Ile Val Val
 35 40 45

2) INFORMATION FOR SEQ ID NO: 43:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 49
 (B) TYPE: AMINO ACID
 (C) STRANDEDNESS: SINGLE
 (D) TOPOLOGY: LINEAR
 (ii) MOLECULE TYPE:

(vi) ORIGINAL SOURCE:
 (A) ORGANISM:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 43:

Glu Trp Gln Thr Asp Asn Cys Glu Thr Cys Thr Cys Tyr Glu Thr Glu
 1 5 10 15
 Ile Ser Cys Cys Thr Leu Val Ser Thr Pro Val Gly Tyr Asp Lys Asp
 20 25 30
 Asn Cys Gln Arg Ile Phe Lys Lys Glu Asp Cys Lys Tyr Ile Val Val
 35 40 45
 Glu

2) INFORMATION FOR SEQ ID NO: 44:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 50
 (B) TYPE: AMINO ACID
 (C) STRANDEDNESS: SINGLE
 (D) TOPOLOGY: LINEAR
 (ii) MOLECULE TYPE:

(vi) ORIGINAL SOURCE:
 (A) ORGANISM:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 44:

Glu Trp Gln Thr Asp Asn Cys Glu Thr Cys Thr Cys Tyr Glu Thr Glu
 1 5 10 15

Ile Ser Cys Cys Thr Leu Val Ser Thr Pro Val Gly Tyr Asp Lys Asp
20 25 30

5 Asn Cys Gln Arg Ile Phe Lys Lys Glu Asp Cys Lys Tyr Ile Val Val
35 40 45

Glu Lys
50

10

2) INFORMATION FOR SEQ ID NO: 45:

(i) SEQUENCE CHARACTERISTICS:

15

- (A) LENGTH: 51
- (B) TYPE: AMINO ACID
- (C) STRANDEDNESS: SINGLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE:

20

(vi) ORIGINAL SOURCE:

(A) ORGANISM:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 45:

25 Glu Trp Gln Thr Asp Asn Cys Glu Thr Cys Thr Cys Tyr Glu Thr Glu
1 5 10 15

Ile Ser Cys Cys Thr Leu Val Ser Thr Pro Val Gly Tyr Asp Lys Asp
20 25 30

30

Asn Cys Gln Arg Ile Phe Lys Lys Glu Asp Cys Lys Tyr Ile Val Val
35 40 45

Glu Lys Lys
50

35

2) INFORMATION FOR SEQ ID NO: 46:

(i) SEQUENCE CHARACTERISTICS:

40

- (A) LENGTH: 52
- (B) TYPE: AMINO ACID
- (C) STRANDEDNESS: SINGLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE:

45

(vi) ORIGINAL SOURCE:

(A) ORGANISM:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 46:

50

Glu Trp Gln Thr Asp Asn Cys Glu Thr Cys Thr Cys Tyr Glu Thr Glu
1 5 10 15

Ile Ser Cys Cys Thr Leu Val Ser Thr Pro Val Gly Tyr Asp Lys Asp
20 25 30

55

Asn Cys Gln Arg Ile Phe Lys Lys Glu Asp Cys Lys Tyr Ile Val Val
35 40 45

Glu Lys Lys Asp
50

60

2) INFORMATION FOR SEQ ID NO: 47:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 53
- (B) TYPE: AMINO ACID
- (C) STRANDEDNESS: SINGLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE:

(vi) ORIGINAL SOURCE:

- (A) ORGANISM:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 47:

Glu Trp Gln Thr Asp Asn Cys Glu Thr Cys Thr Cys Tyr Glu Thr Glu
 1 5 10 15
 Ile Ser Cys Cys Thr Leu Val Ser Thr Pro Val Gly Tyr Asp Lys Asp
 20 25 30
 Asn Cys Gln Arg Ile Phe Lys Lys Glu Asp Cys Lys Tyr Ile Val Val
 35 40 45
 Glu Lys Lys Asp Pro
 50

2) INFORMATION FOR SEQ ID NO: 48:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 54
- (B) TYPE: AMINO ACID
- (C) STRANDEDNESS: SINGLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE:

(vi) ORIGINAL SOURCE:

- (A) ORGANISM:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 48:

Glu Trp Gln Thr Asp Asn Cys Glu Thr Cys Thr Cys Tyr Glu Thr Glu
 1 5 10 15
 Ile Ser Cys Cys Thr Leu Val Ser Thr Pro Val Gly Tyr Asp Lys Asp
 20 25 30
 Asn Cys Gln Arg Ile Phe Lys Lys Glu Asp Cys Lys Tyr Ile Val Val
 35 40 45
 Glu Lys Lys Asp Pro Lys
 50

2) INFORMATION FOR SEQ ID NO: 49:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 55
- (B) TYPE: AMINO ACID
- (C) STRANDEDNESS: SINGLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE:

(vi) ORIGINAL SOURCE:

- (A) ORGANISM:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 49:

Glu Trp Gln Thr Asp Asn Cys Glu Thr Cys Thr Cys Tyr Glu Thr Glu
1 5 10 15
5 Ile Ser Cys Cys Thr Leu Val Ser Thr Pro Val Gly Tyr Asp Lys Asp
20 25 30
Asn Cys Gln Arg Ile Phe Lys Lys Glu Asp Cys Lys Tyr Ile Val Val
35 40 45
10 Glu Lys Lys Asp Pro Lys Lys
50 55

15 2) INFORMATION FOR SEQ ID NO: 50:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 56
(B) TYPE: AMINO ACID
(C) STRANDEDNESS: SINGLE
(D) TOPOLOGY: LINEAR

20

(ii) MOLECULE TYPE:

(vi) ORIGINAL SOURCE:

- (A) ORGANISM:

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 50:

Glu Trp Gln Thr Asp Asn Cys Glu Thr Cys Thr Cys Tyr Glu Thr Glu
1 5 10 15
30 Ile Ser Cys Cys Thr Leu Val Ser Thr Pro Val Gly Tyr Asp Lys Asp
20 25 30
Asn Cys Gln Arg Ile Phe Lys Lys Glu Asp Cys Lys Tyr Ile Val Val
35 35 40 45
Glu Lys Lys Asp Pro Lys Lys Thr
50 55

40

2) INFORMATION FOR SEQ ID NO: 51:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 57
(B) TYPE: AMINO ACID
(C) STRANDEDNESS: SINGLE
(D) TOPOLOGY: LINEAR

45

(ii) MOLECULE TYPE:

(vi) ORIGINAL SOURCE:

- (A) ORGANISM:

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 51:

Glu Trp Gln Thr Asp Asn Cys Glu Thr Cys Thr Cys Tyr Glu Thr Glu
1 5 10 15
55 Ile Ser Cys Cys Thr Leu Val Ser Thr Pro Val Gly Tyr Asp Lys Asp
20 25 30
60 Asn Cys Gln Arg Ile Phe Lys Lys Glu Asp Cys Lys Tyr Ile Val Val
35 40 45

Glu Lys Lys Asp Pro Lys Lys Thr Cys
50 55

5 2) INFORMATION FOR SEQ ID NO: 52:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 58
- (B) TYPE: AMINO ACID
- (C) STRANDEDNESS: SINGLE
- (D) TOPOLOGY: LINEAR

10

(ii) MOLECULE TYPE:

(vi) ORIGINAL SOURCE:

- (A) ORGANISM:

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 52:

Glu Trp Gln Thr Asp Asn Cys Glu Thr Cys Thr Cys Tyr Glu Thr Glu
1 5 10 15

20

Ile Ser Cys Cys Thr Leu Val Ser Thr Pro Val Gly Tyr Asp Lys Asp
20 25 30

25

Asn Cys Gln Arg Ile Phe Lys Lys Glu Asp Cys Lys Tyr Ile Val Val
35 40 45

Glu Lys Lys Asp Pro Lys Lys Thr Cys Ser
50 55

30

2) INFORMATION FOR SEQ ID NO: 53:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 59
- (B) TYPE: AMINO ACID
- (C) STRANDEDNESS: SINGLE
- (D) TOPOLOGY: LINEAR

35

(ii) MOLECULE TYPE:

(vi) ORIGINAL SOURCE:

- (A) ORGANISM:

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 53:

Glu Trp Gln Thr Asp Asn Cys Glu Thr Cys Thr Cys Tyr Glu Thr Glu
1 5 10 15

45

Ile Ser Cys Cys Thr Leu Val Ser Thr Pro Val Gly Tyr Asp Lys Asp
20 25 30

50

Asn Cys Gln Arg Ile Phe Lys Lys Glu Asp Cys Lys Tyr Ile Val Val
35 40 45

Glu Lys Lys Asp Pro Lys Lys Thr Cys Ser Val
50 55

55

2) INFORMATION FOR SEQ ID NO: 54:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60
- (B) TYPE: AMINO ACID

60

(C) STRANDEDNESS: SINGLE
 (D) TOPOLOGY: LINEAR
 (ii) MOLECULE TYPE:

5 (vi) ORIGINAL SOURCE:
 (A) ORGANISM:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 54:

10 Glu Trp Gln Thr Asp Asn Cys Glu Thr Cys Thr Cys Tyr Glu Thr Glu
 1 5 10 15
 Ile Ser Cys Cys Thr Leu Val Ser Thr Pro Val Gly Tyr Asp Lys Asp
 20 25 30
 15 Asn Cys Gln Arg Ile Phe Lys Lys Glu Asp Cys Lys Tyr Ile Val Val
 35 40 45
 20 Glu Lys Lys Asp Pro Lys Lys Thr Cys Ser Val Ser
 50 55 60

2) INFORMATION FOR SEQ ID NO: 55:

25 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 61
 (B) TYPE: AMINO ACID
 (C) STRANDEDNESS: SINGLE
 (D) TOPOLOGY: LINEAR

30 (ii) MOLECULE TYPE:

(vi) ORIGINAL SOURCE:
 (A) ORGANISM:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 55:

35 Glu Trp Gln Thr Asp Asn Cys Glu Thr Cys Thr Cys Tyr Glu Thr Glu
 1 5 10 15
 40 Ile Ser Cys Cys Thr Leu Val Ser Thr Pro Val Gly Tyr Asp Lys Asp
 20 25 30
 Asn Cys Gln Arg Ile Phe Lys Lys Glu Asp Cys Lys Tyr Ile Val Val
 35 40 45
 45 Glu Lys Lys Asp Pro Lys Lys Thr Cys Ser Val Ser Glu
 50 55 60

50 2) INFORMATION FOR SEQ ID NO: 56:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 62
 (B) TYPE: AMINO ACID
 (C) STRANDEDNESS: SINGLE
 55 (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE:

(vi) ORIGINAL SOURCE:
 (A) ORGANISM:

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[illegible]

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Asn Cys Gln Arg Ile Phe Lys Lys Glu Asp Cys Lys Tyr Ile Val Val
 35 40 45
 5 Glu Lys Lys Asp Pro Lys Lys Thr Cys Ser Val Ser Glu Trp Ile Ile
 50 55 60

2) INFORMATION FOR SEQ ID NO: 59:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16
- (B) TYPE: AMINO ACID
- (C) STRANDEDNESS: SINGLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE:

(vi) ORIGINAL SOURCE:

- (A) ORGANISM:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 59:

Ser Glu Trp Gln Thr Asp Asn Cys Glu Thr Cys Thr Cys Tyr Glu Thr
 1 5 10 15

2) INFORMATION FOR SEQ ID NO: 60:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17
- (B) TYPE: AMINO ACID
- (C) STRANDEDNESS: SINGLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE:

(vi) ORIGINAL SOURCE:

- (A) ORGANISM:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 60:

Asn Ser Glu Trp Gln Thr Asp Asn Cys Glu Thr Cys Thr Cys Tyr Glu
 1 5 10 15
 Thr

2) INFORMATION FOR SEQ ID NO: 61:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18
- (B) TYPE: AMINO ACID
- (C) STRANDEDNESS: SINGLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE:

(vi) ORIGINAL SOURCE:

- (A) ORGANISM:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 61:

Ile Asn Ser Glu Trp Gln Thr Asp Asn Cys Glu Thr Cys Thr Cys Tyr
 1 5 10 15
 Glu Thr

2) INFORMATION FOR SEQ ID NO: 62:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19
- (B) TYPE: AMINO ACID
- (C) STRANDEDNESS: SINGLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE:

(vi) ORIGINAL SOURCE:

- (A) ORGANISM:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 62:

Pro Ile Asn Ser Glu Trp Gln Thr Asp Asn Cys Glu Thr Cys Thr Cys
 1 5 10 15

Tyr Glu Thr

2) INFORMATION FOR SEQ ID NO: 63:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20
- (B) TYPE: AMINO ACID
- (C) STRANDEDNESS: SINGLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE:

(vi) ORIGINAL SOURCE:

- (A) ORGANISM:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 63:

His Pro Ile Asn Ser Glu Trp Gln Thr Asp Asn Cys Glu Thr Cys Thr
 1 5 10 15

Cys Tyr Glu Thr
 20

2) INFORMATION FOR SEQ ID NO: 64:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21
- (B) TYPE: AMINO ACID
- (C) STRANDEDNESS: SINGLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE:

(vi) ORIGINAL SOURCE:

- (A) ORGANISM:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 64:

Lys His Pro Ile Asn Ser Glu Trp Gln Thr Asp Asn Cys Glu Thr Cys
 1 5 10 15

Thr Cys Tyr Glu Thr
 20

2) INFORMATION FOR SEQ ID NO: 65:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22
- (B) TYPE: AMINO ACID
- (C) STRANDEDNESS: SINGLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE:

(vi) ORIGINAL SOURCE:

- (A) ORGANISM:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 65:

Asn Lys His Pro Ile Asn Ser Glu Trp Gln Thr Asp Asn Cys Glu Thr
 1 5 10 15
 Cys Thr Cys Tyr Glu Thr
 20

2) INFORMATION FOR SEQ ID NO: 66:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23
- (B) TYPE: AMINO ACID
- (C) STRANDEDNESS: SINGLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE:

(vi) ORIGINAL SOURCE:

- (A) ORGANISM:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 66:

Gly Asn Lys His Pro Ile Asn Ser Glu Trp Gln Thr Asp Asn Cys Glu
 1 5 10 15
 Thr Cys Thr Cys Tyr Glu Thr
 20

2) INFORMATION FOR SEQ ID NO: 67:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24
- (B) TYPE: AMINO ACID
- (C) STRANDEDNESS: SINGLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE:

(vi) ORIGINAL SOURCE:

- (A) ORGANISM:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 67:

Lys Gly Asn Lys His Pro Ile Asn Ser Glu Trp Gln Thr Asp Asn Cys
 1 5 10 15
 Glu Thr Cys Thr Cys Tyr Glu Thr
 20

2) INFORMATION FOR SEQ ID NO: 68:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25
(B) TYPE: AMINO ACID
(C) STRANDEDNESS: SINGLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE:

(vi) ORIGINAL SOURCE:

- (A) ORGANISM:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 68:

15 Leu Lys Gly Asn Lys His Pro Ile Asn Ser Glu Trp Gln Thr Asp Asn
1 5 10 15
Cys Glu Thr Cys Thr Cys Tyr Glu Thr
20 25

2) INFORMATION FOR SEQ ID NO: 69:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26
(B) TYPE: AMINO ACID
(C) STRANDEDNESS: SINGLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE:

(vi) ORIGINAL SOURCE:

- (A) ORGANISM:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 69:

35 Asp Leu Lys Gly Asn Lys His Pro Ile Asn Ser Glu Trp Gln Thr Asp
1 5 10 15
Asn Cys Glu Thr Cys Thr Cys Tyr Glu Thr
20 25

2) INFORMATION FOR SEQ ID NO: 70:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27
(B) TYPE: AMINO ACID
(C) STRANDEDNESS: SINGLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE:

(vi) ORIGINAL SOURCE:

- (A) ORGANISM:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 70:

55 Met Asp Leu Lys Gly Asn Lys His Pro Ile Asn Ser Glu Trp Gln Thr
1 5 10 15
Asp Asn Cys Glu Thr Cys Thr Cys Tyr Glu Thr
20 25

2) INFORMATION FOR SEQ ID NO: 71:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28
- (B) TYPE: AMINO ACID
- (C) STRANDEDNESS: SINGLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE:

(vi) ORIGINAL SOURCE:

- (A) ORGANISM:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 71:

Cys Met Asp Leu Lys Gly Asn Lys His Pro Ile Asn Ser Glu Trp Gln
 1 5 10 15
 Thr Asp Asn Cys Glu Thr Cys Thr Cys Tyr Glu Thr
 20 25

2) INFORMATION FOR SEQ ID NO: 72:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29
- (B) TYPE: AMINO ACID
- (C) STRANDEDNESS: SINGLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE:

(vi) ORIGINAL SOURCE:

- (A) ORGANISM:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 72:

Lys Cys Met Asp Leu Lys Gly Asn Lys His Pro Ile Asn Ser Glu Trp
 1 5 10 15
 Gln Thr Asp Asn Cys Glu Thr Cys Thr Cys Tyr Glu Thr
 20 25

2) INFORMATION FOR SEQ ID NO: 73:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30
- (B) TYPE: AMINO ACID
- (C) STRANDEDNESS: SINGLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE:

(vi) ORIGINAL SOURCE:

- (A) ORGANISM:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 73:

Arg Lys Cys Met Asp Leu Lys Gly Asn Lys His Pro Ile Asn Ser Glu
 1 5 10 15
 Trp Gln Thr Asp Asn Cys Glu Thr Cys Thr Cys Tyr Glu Thr
 20 25 30

2) INFORMATION FOR SEQ ID NO: 74:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 31
 (B) TYPE: AMINO ACID
 (C) STRANDEDNESS: SINGLE
 (D) TOPOLOGY: LINEAR
 5 (ii) MOLECULE TYPE:
 (vi) ORIGINAL SOURCE:
 (A) ORGANISM:
 10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 74:
 Thr Arg Lys Cys Met Asp Leu Lys Gly Asn Lys His Pro Ile Asn Ser
 1 5 10 15
 15 Glu Trp Gln Thr Asp Asn Cys Glu Thr Cys Thr Cys Tyr Glu Thr
 20 25 30
 2) INFORMATION FOR SEQ ID NO: 75:
 20 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 32
 (B) TYPE: AMINO ACID
 (C) STRANDEDNESS: SINGLE
 (D) TOPOLOGY: LINEAR
 25 (ii) MOLECULE TYPE:
 (vi) ORIGINAL SOURCE:
 (A) ORGANISM:
 30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 75:
 Ser Thr Arg Lys Cys Met Asp Leu Lys Gly Asn Lys His Pro Ile Asn
 1 5 10 15
 35 Ser Glu Trp Gln Thr Asp Asn Cys Glu Thr Cys Thr Cys Tyr Glu Thr
 20 25 30
 2) INFORMATION FOR SEQ ID NO: 76:
 40 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 33
 (B) TYPE: AMINO ACID
 (C) STRANDEDNESS: SINGLE
 (D) TOPOLOGY: LINEAR
 45 (ii) MOLECULE TYPE:
 (vi) ORIGINAL SOURCE:
 (A) ORGANISM:
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 76:
 50 Asp Ser Thr Arg Lys Cys Met Asp Leu Lys Gly Asn Lys His Pro Ile
 1 5 10 15
 55 Asn Ser Glu Trp Gln Thr Asp Asn Cys Glu Thr Cys Thr Cys Tyr Glu
 20 25 30
 Thr
 2) INFORMATION FOR SEQ ID NO: 77:
 60 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 34

(B) TYPE: AMINO ACID
(C) STRANDEDNESS: SINGLE
(D) TOPOLOGY: LINEAR
(ii)MOLECULE TYPE:

5

(vi)ORIGINAL SOURCE:
(A) ORGANISM:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 77:

10

Gly Asp Ser Thr Arg Lys Cys Met Asp Leu Lys Gly Asn Lys His Pro
1 5 10 15

15

Ile Asn Ser Glu Trp Gln Thr Asp Asn Cys Glu Thr Cys Thr Cys Tyr
20 25 30

Glu Thr

2) INFORMATION FOR SEQ ID NO: 78:

20

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 35
(B) TYPE: AMINO ACID
(C) STRANDEDNESS: SINGLE
(D) TOPOLOGY: LINEAR

25

(ii)MOLECULE TYPE:

(vi)ORIGINAL SOURCE:
(A) ORGANISM:

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 78:

Pro Gly Asp Ser Thr Arg Lys Cys Met Asp Leu Lys Gly Asn Lys His
1 5 10 15

35

Pro Ile Asn Ser Glu Trp Gln Thr Asp Asn Cys Glu Thr Cys Thr Cys
20 25 30

Tyr Glu Thr
35

40

2) INFORMATION FOR SEQ ID NO: 79:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 36
(B) TYPE: AMINO ACID
(C) STRANDEDNESS: SINGLE
(D) TOPOLOGY: LINEAR

45

(ii)MOLECULE TYPE:

(vi)ORIGINAL SOURCE:
(A) ORGANISM:

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 79:

Val Pro Gly Asp Ser Thr Arg Lys Cys Met Asp Leu Lys Gly Asn Lys
1 5 10 15

55

His Pro Ile Asn Ser Glu Trp Gln Thr Asp Asn Cys Glu Thr Cys Thr
20 25 30

Cys Tyr Glu Thr

60

35

2) INFORMATION FOR SEQ ID NO: 80:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37
- (B) TYPE: AMINO ACID
- (C) STRANDEDNESS: SINGLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE:

(vi) ORIGINAL SOURCE:

- (A) ORGANISM:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 80:

Gly Val Pro Gly Asp Ser Thr Arg Lys Cys Met Asp Leu Lys Gly Asn
 1 5 10 15
 Lys His Pro Ile Asn Ser Glu Trp Gln Thr Asp Asn Cys Glu Thr Cys
 20 25 30
 Thr Cys Tyr Glu Thr
 35

2) INFORMATION FOR SEQ ID NO: 81:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 38
- (B) TYPE: AMINO ACID
- (C) STRANDEDNESS: SINGLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE:

(vi) ORIGINAL SOURCE:

- (A) ORGANISM:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 81:

Glu Gly Val Pro Gly Asp Ser Thr Arg Lys Cys Met Asp Leu Lys Gly
 1 5 10 15
 Asn Lys His Pro Ile Asn Ser Glu Trp Gln Thr Asp Asn Cys Glu Thr
 20 25 30
 Cys Thr Cys Tyr Glu Thr
 35

2) INFORMATION FOR SEQ ID NO: 82:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39
- (B) TYPE: AMINO ACID
- (C) STRANDEDNESS: SINGLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE:

(vi) ORIGINAL SOURCE:

- (A) ORGANISM:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 82:

Asn Glu Gly Val Pro Gly Asp Ser Thr Arg Lys Cys Met Asp Leu Lys
 1 5 10 15

Gly Asn Lys His Pro Ile Asn Ser Glu Trp Gln Thr Asp Asn Cys Glu
 20 25 30
 Thr Cys Thr Cys Tyr Glu Thr
 5 35

2) INFORMATION FOR SEQ ID NO: 83:

10 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 40
 (B) TYPE: AMINO ACID
 (C) STRANDEDNESS: SINGLE
 (D) TOPOLOGY: LINEAR

15 (ii) MOLECULE TYPE:

(vi) ORIGINAL SOURCE:
 (A) ORGANISM:

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 83:

Pro Asn Glu Gly Val Pro Gly Asp Ser Thr Arg Lys Cys Met Asp Leu
 1 5 10 15
 25 Lys Gly Asn Lys His Pro Ile Asn Ser Glu Trp Gln Thr Asp Asn Cys
 20 25 30
 Glu Thr Cys Thr Cys Tyr Glu Thr
 35 40

30 2) INFORMATION FOR SEQ ID NO: 84:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 41
 (B) TYPE: AMINO ACID
 (C) STRANDEDNESS: SINGLE
 (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE:

(vi) ORIGINAL SOURCE:
 (A) ORGANISM:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 84:

Ile Pro Asn Glu Gly Val Pro Gly Asp Ser Thr Arg Lys Cys Met Asp
 1 5 10 15
 Leu Lys Gly Asn Lys His Pro Ile Asn Ser Glu Trp Gln Thr Asp Asn
 20 25 30
 Cys Glu Thr Cys Thr Cys Tyr Glu Thr
 50 35 40

55 2) INFORMATION FOR SEQ ID NO: 85:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 42
 (B) TYPE: AMINO ACID
 (C) STRANDEDNESS: SINGLE
 (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE:

(vi) ORIGINAL SOURCE:

(A) ORGANISM:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 85:

5

Phe Ile Pro Asn Glu Gly Val Pro Gly Asp Ser Thr Arg Lys Cys Met
1 5 10 15

10

Asp Leu Lys Gly Asn Lys His Pro Ile Asn Ser Glu Trp Gln Thr Asp
20 25 30

Asn Cys Glu Thr Cys Thr Cys Tyr Glu Thr
35 40

15

2) INFORMATION FOR SEQ ID NO: 86:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 43

(B) TYPE: AMINO ACID

(C) STRANDEDNESS: SINGLE

20

(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE:

(vi) ORIGINAL SOURCE:

(A) ORGANISM:

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 86:

Tyr Phe Ile Pro Asn Glu Gly Val Pro Gly Asp Ser Thr Arg Lys Cys
1 5 10 15

30

Met Asp Leu Lys Gly Asn Lys His Pro Ile Asn Ser Glu Trp Gln Thr
20 25 30

Asp Asn Cys Glu Thr Cys Thr Cys Tyr Glu Thr
35 40

35

2) INFORMATION FOR SEQ ID NO: 87:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 44

(B) TYPE: AMINO ACID

(C) STRANDEDNESS: SINGLE

(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE:

45

(vi) ORIGINAL SOURCE:

(A) ORGANISM:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 87:

50

Cys Tyr Phe Ile Pro Asn Glu Gly Val Pro Gly Asp Ser Thr Arg Lys
1 5 10 15

Cys Met Asp Leu Lys Gly Asn Lys His Pro Ile Asn Ser Glu Trp Gln
20 25 30

55

Thr Asp Asn Cys Glu Thr Cys Thr Cys Tyr Glu Thr
35 40

2) INFORMATION FOR SEQ ID NO: 88:

60

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 45
 (C) TYPE: AMINO ACID
 (C) STRANDEDNESS: SINGLE
 (D) TOPOLOGY: LINEAR
 5 (ii)MOLECULE TYPE:
 (vi)ORIGINAL SOURCE:
 (A) ORGANISM:
 10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 88:

Ser Cys Tyr Phe Ile Pro Asn Glu Gly Val Pro Gly Asp Ser Thr Arg
 1 5 10 15
 15 Lys Cys Met Asp Leu Lys Gly Asn Lys His Pro Ile Asn Ser Glu Trp
 20 25 30
 Gln Thr Asp Asn Cys Glu Thr Cys Thr Cys Tyr Glu Thr
 35 40 45

20

2) INFORMATION FOR SEQ ID NO: 89:

25 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 15
 (B) TYPE: AMINO ACID
 (C) STRANDEDNESS: SINGLE
 (D) TOPOLOGY: LINEAR
 (ii)MOLECULE TYPE:
 30 (ix) FEATURE :
 (A) NAME/KEY : Modified site
 (B) LOCATION : 1
 (D) OTHER INFORMATION : The residue in this
 35 position is either glutamic acid, asparagine, or
 aspartic acid.
 (ix) FEATURE :
 (A) NAME/KEY : Modified site
 (B) LOCATION : 4
 (D)OTHER INFORMATION : The residue in this position
 40 is either threonine, or serine.
 (ix) FEATURE :
 (A) NAME/KEY : Modified site
 (B) LOCATION : 6
 (D)OTHER INFORMATION : The residue in this position
 45 is either glutamic acid, asparagine, or aspartic
 acid.
 (ix) FEATURE :
 (A) NAME/KEY : Modified site
 (B) LOCATION : 8
 (D)OTHER INFORMATION : The residue in this position
 50 is either glutamic acid, asparagine, or aspartic
 acid.
 (ix) FEATURE :
 (A)NAME/KEY : Modified site
 (B)LOCATION : 9
 (D)OTHER INFORMATION : The residue in this position
 55 is either threonine, or serine.
 (ix) FEATURE :
 (A)NAME/KEY : Modified site
 (B)LOCATION : 11
 (D)OTHER INFORMATION : The residue in this position
 60 is either threonine, or serine.
 (ix) FEATURE :
 (A)NAME/KEY : Modified site

(B)LOCATION : 13
(D)OTHER INFORMATION : The residue in this position
is either tyrosine, or phenylalanine.

(ix) FEATURE :

(A)NAME/KEY : Modified site

(B)LOCATION : 14

(D)OTHER INFORMATION : The residue in this position
is either glutamic acid, asparagine, or aspartic
acid.

(ix) FEATURE :

(A)NAME/KEY : Modified site

(B)LOCATION : 15

(D)OTHER INFORMATION : The residue in this position
is either threonine, or serine.

(vi)ORIGINAL SOURCE:

(A) ORGANISM:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 89:

Xaa Trp Gln Xaa Asp Xaa Cys Xaa Xaa Cys Xaa Cys Xaa Xaa Xaa
1 5 10 15

2) INFORMATION FOR SEQ ID NO: 90:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 30

(B) TYPE: AMINO ACID

(C) STRANDEDNESS: SINGLE

(D) TOPOLOGY: LINEAR

(ii)MOLECULE TYPE:

(vi)ORIGINAL SOURCE:

(A) ORGANISM:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 90:

Glu Trp Gln Thr Asp Asn Cys Glu Thr Cys Thr Cys Tyr Glu Thr Glu
1 5 10 15

Trp Gln Thr Asp Asn Cys Glu Thr Cys Thr Cys Tyr Glu Thr
20 25 30

2) INFORMATION FOR SEQ ID NO: 91:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 45

(B) TYPE: AMINO ACID

(C) STRANDEDNESS: SINGLE

(D) TOPOLOGY: LINEAR

(ii)MOLECULE TYPE:

(vi)ORIGINAL SOURCE:

(A) ORGANISM:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 91:

Glu Trp Gln Thr Asp Asn Cys Glu Thr Cys Thr Cys Tyr Glu Thr Glu
 1 5 10 15

5 Trp Gln Thr Asp Asn Cys Glu Thr Cys Thr Cys Tyr Glu Thr Glu Trp
 20 25 30

Gln Thr Asp Asn Cys Glu Thr Cys Thr Cys Tyr Glu Thr
 35 40 45

10

2) INFORMATION FOR SEQ ID NO: 92:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 60

(B) TYPE: AMINO ACID

15 (C) STRANDEDNESS: SINGLE

(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE:

(vi) ORIGINAL SOURCE:

20 (A) ORGANISM:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 92:

25 Glu Trp Gln Thr Asp Asn Cys Glu Thr Cys Thr Cys Tyr Glu Thr Glu
 1 5 10 15

Trp Gln Thr Asp Asn Cys Glu Thr Cys Thr Cys Tyr Glu Thr Glu Trp
 20 25 30

30 Gln Thr Asp Asn Cys Glu Thr Cys Thr Cys Tyr Glu Thr Glu Trp Gln
 35 40 45

Thr Asp Asn Cys Glu Thr Cys Thr Cys Tyr Glu Thr
 50 55 60

35